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132260

mg

From: Huff, Sheela  
Sent: Monday, September 13, 2004 5:58 AM  
To: STIC-Biotech/ChemLib  
Subject: search request for 10042347

Please search and interference search SEQ ID No. 4 of the above application.

Thanks

Sheela Huff  
Art Unit 1642  
571-272-0834  
Remsen 3A15  
mailbox Remsen 3C18

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 18:25:17 ; Search time 78 Seconds  
(without alignments)  
3884.656 Million cell updates/sec

Title: US-10-042-347-4

Perfect score: 546  
Sequence: 1 caccgcaccgcagcttccca.....acagcttcacgacgtctcc 546

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*  
1: /cgn2\_6/prodata/2/ina/5A COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/6A COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCUS COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	546	US-09-315-689-4	Sequence 4, Appli
2	546	100.0	552	US-09-206-059-30	Sequence 30, Appli
3	546	100.0	563	US-09-231-077D-9	Sequence 9, Appli
4	546	100.0	3394	US-08-159-784-4	Sequence 4, Appli
5	534	97.8	534	US-09-315-689-4	Sequence 6, Appli
6	381.2	69.8	558	US-09-449-293-3	Sequence 3, Appli
7	381.2	69.8	558	US-09-775-325-3	Sequence 3, Appli
8	381.2	69.8	558	US-09-775-174-3	Sequence 3, Appli
9	381.2	69.8	558	US-08-985-526-37	Sequence 37, Appli
10	381.2	69.8	573	US-09-561-500-12	Sequence 12, Appli
11	381.2	69.8	573	US-09-561-108-12	Sequence 12, Appli
12	381.2	69.8	573	US-09-561-526-12	Sequence 12, Appli
13	381.2	69.8	573	US-09-561-499-12	Sequence 12, Appli
14	381.2	69.8	573	US-09-998-831-12	Sequence 12, Appli
15	381.2	69.8	620	US-09-231-077D-5	Sequence 5, Appli
16	379.6	69.5	568	US-09-231-077D-8	Sequence 8, Appli
17	379.6	69.5	580	US-09-231-077D-7	Sequence 7, Appli
18	379.6	69.5	4031	US-08-159-784-1	Sequence 1, Appli
19	378	69.2	582	US-09-231-077D-6	Sequence 6, Appli
20	60	11.0	79	US-09-231-077D-4	Sequence 4, Appli
21	57	10.4	71	US-09-231-077D-3	Sequence 3, Appli
22	46.6	8.5	1467	US-09-252-991A-1632	Sequence 1632, Ap
23	46.6	8.5	2025	US-09-252-991A-1536	Sequence 1536, Ap
24	46	8.4	1038	US-09-252-991A-9197	Sequence 8667, Ap
25	46	8.4	1410	US-09-252-991A-8867	Sequence 9114, Ap
26	46	8.4	2067	US-09-252-991A-9114	Sequence 8976, Ap
27	46	8.4	2634	US-09-252-991A-8976	

28	45.6	8.4	2451	US-09-252-991A-7534	Sequence 7534, Ap
29	45.6	8.4	2651	US-09-252-991A-7807	Sequence 7807, Ap
30	45.6	8.4	2868	US-09-252-991A-7683	Sequence 7683, Ap
31	45.4	8.3	498	US-09-252-991A-15905	Sequence 15905, A
32	45.4	8.3	522	US-09-252-991A-15788	Sequence 15788, A
33	45.4	8.3	1101	US-09-252-991A-15814	Sequence 15814, A
34	45.4	8.3	1887	US-09-252-991A-15843	Sequence 15843, A
35	45.4	8.3	2103	US-09-252-991A-15876	Sequence 15876, A
36	44.8	8.2	1206	US-09-252-991A-3667	Sequence 3667, Ap
37	44.8	8.2	1320	US-09-252-991A-3779	Sequence 2103, Ap
38	44.4	8.1	1116	US-09-252-991A-2102	Sequence 1793, Ap
39	44.4	8.1	1224	US-09-252-991A-1793	Sequence 52, Appl
40	44.4	8.1	3113	US-09-894-998A-52	Sequence 48, Appl
41	44	8.1	3350	US-09-894-998A-48	Sequence 14, Appl
42	43.6	8.0	1686	US-08-646-657-14	Sequence 3, Appli
43	43.6	8.0	1794	PCT-US95-14418-3	Sequence 3, Appli
44	43.6	8.0	1794	PCT-US95-15327-3	Sequence 3, Appli
45	43.6	8.0	2499	US-09-758-282B-94	Sequence 94, Appl

## ALIGNMENTS

RESULT 1  
US-09-315-689-4  
Sequence 4, Application US/09315689  
Patent No. 6346510  
GENERAL INFORMATION:  
APPLICANT: Folkman, Judah  
APPLICANT: O'Reilly, Michael  
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions  
FILE REFERENCE: 05213-0228  
CURRENT APPLICATION NUMBER: US/09/315, 689  
CURRENT FILING DATE: 1999-05-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 546  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-315-689-4

Query Match 100.0%; Score 546; DB 4; Length 546;  
Best Local Similarity 100.0%; Pred. No. 8.1e-113;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CACAGCCACCGGACCTTCCAGCCGAGTCTCACTGTTGGCTCAACAGCCCTGTCA	60
DB	1	CAAGCCACCGGACCTTCCAGCCGAGTCTCACTGTTGGCTCAACAGCCCTGTCA	60
QY	61	GCGCGCATGCGGCGATCCGCGGCGCGGCGGCTTCCAGGAGCGCGGCGGTG	120
DB	61	GCGCGCATGCGGCGATCCGCGGCGCGGCGGCTTCCAGGAGCGCGGCGGTG	120
QY	121	GCGCGCGGCGGACCTTCCGCGGCGGCTTCCAGGAGCGCGGCGGTG	180
DB	121	GCGCGCGGCGGACCTTCCGCGGCGGCTTCCAGGAGCGCGGCGGTG	180
QY	181	GCGCGCGGCGGACCTTCCGCGGCGGCTTCCAGGAGCGCGGCGGTG	240
DB	181	GCGCGCGGCGGACCTTCCGCGGCGGCTTCCAGGAGCGCGGCGGTG	240
QY	241	CCAGCTGAGGAGCTTCTTCAAGGCTTCAAGGCTTCAAGGAGCTTCAAGGAGCTT	300
DB	241	CCAGCTGAGGAGCTTCTTCAAGGCTTCAAGGCTTCAAGGAGCTTCAAGGAGCTT	300
QY	301	TTTCTCTTTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTT	360
DB	301	TTTCTCTTTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTT	360
QY	361	CATGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTT	420
DB	361	CATGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAGCTT	420

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QUESTION**

QY	1	CAAGGCAACCGCACTTCCAGCCGATCTCAACCTGGTATGGCTCAACAGCCCTCTTA	60
Db	6	CAGAAGCAACGCGCACTTCCAGCCGATCTCAACCTGGTATGGCTCAACAGCCCTCTTA	65
QY	61	GGGCGCATGCGGGCAATCCGCGGGGCGCACTTCAGTCTTCCAGCAGGCGCGGCGGTG	120
Db	66	GGGCGCATGCGGGGCACTCCGCGGGGCGCACTTCAGTCTTCCAGCAGGCGCGGCGGTG	125
QY	121	GGGCTGAGGGGCACTTCCGCGGCTTCTGTTCTCTGGCTCGGCGCTGAGGACCTGTACAGATC	180
Db	126	GGGCTGAGGGGCACTTCCGCGGCTTCTGTTCTCTGGCTCGGCGCTGAGGACCTGTACAGATC	185
QY	181	GTGCGCGGTGCGCAACGCGCAGCGTGGCCATGTAACCTCAAGGACGAACTGCTTT	240
Db	186	GTGCGCGGTGCGCAACGCGCAGCGTGGCCATGTAACCTCAAGGACGAACTGCTTT	245
QY	241	CCGAGTGGAGGCTCTGTCTCAGGCTCTGAGGGTCCGCTGAAAGCCGGGGACAGCATC	300
Db	246	CCGAGTGGAGGCTCTGTCTCAGGCTCTGAGGGTCCGCTGAAAGCCGGGGACAGCATC	305
QY	301	TTTCTCTTTAAGGCAAGGATGTTCTGAAGGCACTCCCACTGGGCCCAAGAGCGGTGTG	360
Db	306	TTTCTCTTTAAGGCAAGGATGTTCTGAAGGCACTCCCACTGGGCCCAAGAGCGGTGTG	365
QY	361	CATGGCTTCGAGCCCAAGGAGGCGGAGGCTGACCGAAGCTACCTGTGAACCTGAGCGAAG	420
Db	366	CATGGCTTCGAGCCCAAGGAGGCGGAGGCTGACCGAAGCTACCTGTGAACCTGAGCGAAG	425
QY	421	GAGGCTCCCTCGCAACGAGGCAAGGCTCTCGTCTGTGGGGGGAGGCTCTCGGGGAG	490
Db	426	GAGGCTCCCTCGGCAACGAGGCAAGGCTCTCGTCTGTGGGGGGAGGCTCTCGGGGAG	485
QY	481	AATGGCGGAGCTGCCATCAAGCTTACATGTTCTGTGATTTAGAAACAAGCTTCAATGCT	540
Db	486	AATGGCGGAGCTGCCATCAAGCTTACATGTTCTGTGATTTAGAAACAAGCTTCAATGCT	545
QY	541	GGCTCC	546
Db	546	GGCTCC	551



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RESULT 6
US-09-449-293-3
; Sequence 3, Application US/09449293
; Patent No. 6267954
; GENERAL INFORMATION:
; APPLICANT: Abitbol, Marc
; APPLICANT: Uteza, Yves
; APPLICANT: Menasche, Maurice
; APPLICANT: Bossard, Carine
; APPLICANT: Van Den Bergh, Loic
; APPLICANT: Bonnel, Sebastien
; APPLICANT: Prats, Hervé
; APPLICANT: Honinger, Jiri
; APPLICANT: Neuner-Jehle, Martin
; TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
; FILE REFERENCE: 8076.202US01
; CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: US/09/449,293
; SOFTWARE: Patentin Ver. 2.0
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 3
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-449-293-3

Query Match      69.8%; Score 381.2; DB 3; Length 558;
Best Local Similarity 81.1%; Pred. No. 3.1e-76;
Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGCTGCTCCACCTGTTGCGCTTAACAGCCCCCTGTCA 60
DB 4 CATACCTATCAGACCTTTTCCAGCACTGCTCCACCTGTTGCGCTTAACAGCCCCCTGTCT 63
QY 61 GCGCGCATGCGGCGCATCCCGGGCCGACCTTCCAGTGTTCACAGCGCGCGCGT 120
DB 64 GAGGACATGCGTGTATCCGTGACAGATTCCTCAAGTGTTCACAGCGCGCGCGT 123
QY 121 GGGCTGCGGCGGACCTTCCGCGCTTCTGCTCCGCGCTGCGAGACCTGTACAGCATC 180
DB 124 GGGCTGCGGCGGACCTTCCGCGCTTCTGCTCCGCGCTGCGAGATCTTATAGCATC 183
QY 181 GTGCGCGCTGCGGACCGCGAGCGGCTGCTCAACTCAAGAGCGAGCTGTCTT 240
DB 184 GTGCGCGCTGCGGACCGCGGCGTGTGCGCATGTGTAAGTGAAGAGCGAGTCTATCT 243
QY 241 CCGAGCTGAGAGGCTGTCTGAGGCTTGAAGGTCGCTGAAGCCCGGGGACGCAATC 300
DB 244 CCGAGCTGAGAGTCCCTGTGTTTCTGCTCCAGGCTCAACTGCAACCCGGGGCCGCAATC 303
QY 301 TTCTCTTTTGAAGGCAAGGACGCTCTGAGGCAACCCGAGCTGCGGCGGAGAGCTGTGG 360
DB 304 TTTTCTTTTGAAGGCAAGATGTCTTGAAGACCCGAGCTGCGGCGGAGAGGCTATGG 363
QY 361 CATGCTGAGACCCCAAGCGGCGAGGCTGACCGAGCTACTGTGAGAGCTGTGCGAGC 420
DB 364 CAGGCTGAGACCCCAAGCGGCGAGGCTGATGAGAGATTTCTGTGAGACATGAGGAACT 423
QY 421 GAGGCTCTCTGCGGCGAGCGGCGAGGCTCTGCTGCTGCTGCGGGGCGAGGCTCTGAGGAG 480
DB 424 GAAACTACTGAGGCTGACAGGCTCCTCTGCTGCTGCTGCTGAGGAGGCTCTGGAACAG 483
QY 481 AGTCCGCGAGCTGCGCATCAGCTTACATGCTGTGAGAGAGAGCTTATGACT 540
DB 484 AAAGCTGCGAGCTGCGCAACAAGCTATGCTGTGAGAGAGATGCTTATGACC 543
QY 541 GCTTCC 546
DB 544 TCTTTC 549
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RESULT 7
US-09-775-325-3
; Sequence 3, Application US/09775325
; Patent No. 6500449
; GENERAL INFORMATION:
; APPLICANT: Abitbol, Marc
; APPLICANT: Uteza, Yves
; APPLICANT: Menasche, Maurice
; APPLICANT: Bossard, Carine
; APPLICANT: Van Den Bergh, Loic
; APPLICANT: Bonnel, Sebastian
; APPLICANT: Prats, Hervé
; APPLICANT: Honinger, Jiri
; APPLICANT: Neuner-Jehle, Martin
; TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
; FILE REFERENCE: 8076.202USD1
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 09/449,293
; SOFTWARE: Patentin version 3.1
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 3
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-775-325-3

Query Match      69.8%; Score 381.2; DB 4; Length 558;
Best Local Similarity 81.1%; Pred. No. 3.1e-76;
Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGCTGCTCCACCTGTTGCGCTTAACAGCCCCCTGTCA 60
DB 4 CATACCTATCAGACCTTTTCCAGCACTGCTCCACCTGTTGCGCTTAACAGCCCCCTGTCT 63
QY 61 GCGCGCATGCGGCGCATCCCGGGCCGACCTTCCAGTGTTCACAGCGCGCGCGT 120
DB 64 GAGGACATGCGTGTATCCGTGACAGATTCCTCAAGTGTTCACAGCGCGCGCGT 123
QY 121 GGGCTGCGGCGGACCTTCCGCGCTTCTGCTCCGCGCTGCGAGACCTGTACAGCATC 180
DB 124 GGGCTGCGGCGGACCTTCCGCGCTTCTGCTCCGCGCTGCGAGATCTTATAGCATC 183
QY 181 GTGCGCGCTGCGGACCGCGAGCGGCTGCTCAACTCAAGAGCGAGCTGTCTT 240
DB 184 GTGCGCGCTGCGGACCGCGGCGTGTGCGCATGTGTAAGTGAAGAGAGTCTATCT 243
QY 241 CCGAGCTGAGAGGCTGTCTGAGGCTTGAAGGTCGCTGAAGCCCGGGGACGCAATC 300
DB 244 CCGAGCTGAGAGTCCCTGTGTTTCTGCTCCAGGCTCAACTGCAACCCGGGGCCGCAATC 303
QY 301 TTCTCTTTTGAAGGCAAGGACGCTCTGAGGCAACCCGAGCTGCGGCGGAGAGCTGTGG 360
DB 304 TTTTCTTTTGAAGGCAAGATGTCTTGAAGACCCGAGCTGCGGCGGAGAGGCTATGG 363
QY 361 CATGCTGAGACCCCAAGCGGCGAGGCTGACCGAGCTACTGTGAGAGCTGTGCGAGC 420
DB 364 CAGGCTGAGACCCCAAGCGGCGAGGCTGATGAGAGATTTCTGTGAGACATGAGGAACT 423
QY 421 GAGGCTCTCTGCGGCGAGCGGCGAGGCTCTGCTGCTGCTGCGGGGCGAGGCTCTGAGGAG 480
DB 424 GAAACTACTGAGGCTGACAGGCTCCTCTGCTGCTGCTGCTGAGGAGGCTCTGGAACAG 483
QY 481 AGTCCGCGAGCTGCGCATCAGCTTACATGCTGTGAGAGAGAGCTTATGACT 540
DB 484 AAAGCTGCGAGCTGCGCAACAAGCTATGCTGTGAGAGAGATGCTTATGACC 543
QY 541 GCTTCC 546
DB 544 TCTTTC 549
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## RESULT 8

US-09-775-174-3  
 ; Sequence 3, Application US/09775174  
 ; Patent No. 6663894  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aditpol, Marc  
 ; APPLICANT: Uteza, Yves  
 ; APPLICANT: Menasche, Maurice  
 ; APPLICANT: Bossard, Carine  
 ; APPLICANT: Van Den Bergh, Loic  
 ; APPLICANT: Bonnel, Sebastien  
 ; APPLICANT: Prats, Hervé  
 ; APPLICANT: Honiger, Jiri  
 ; APPLICANT: Neuner-Jehle, Martin  
 ; TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS  
 ; FILE REFERENCE: 8076.202USD2  
 ; CURRENT APPLICATION NUMBER: US/09/775,174  
 ; CURRENT FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: US 09/449,293  
 ; PRIOR FILING DATE: 1999-11-24  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 558  
 ; TYPE: DNA  
 ; ORGANISM: Rattus rattus  
 ; US-09-775-174-3

Query Match 69.8%; Score 381.2; DB 4; Length 558;  
 Best Local Similarity 81.1%; Pred. No. 3.1e-76;  
 Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

1 CACAGCCGCGGACCTTCCAGCCGGTGTCTCACTGTTGGGCTCAACAGCCCTCTGCA 60  
 4 CATCTCATCAGACTTTTACGACTGTCTCACTGTGTGGACACTGAACACCCCTGTCT 63  
 61 GGCAGCATGCGGGGCAATCGCGGGGCGCACTTCAGTGTCTCAAGCGCGGGCCGTG 120  
 64 GGAAGCATGCGGTGTATTCGTGTGAGAGATTTTCAGTGTCTTCAGCAAGCGCGGCGTG 123  
 121 GGGCTGGGGGCACTTTCGCGGCTTCTGTCTCTGCGGCTGTGAGAGACTGTACAGATC 180  
 124 GGGCTGTGGGCACTTTCGCGGCTTCTGTCTCTGTGAGAGACTGTACAGATC 183  
 181 GTGGCGGCTGTGAGAGCGGCGGCGGCTGTGAGAGACTGTACAGATC 240  
 184 GTGGCGGCTGTGAGAGCGGCGGCGGCTGTGAGAGACTGTACAGATC 243  
 241 CCCAGCTGGAGGCTCTGTCTCAAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 300  
 244 CCCAGCTGGAGCTCTGTCTCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 303  
 301 TTCTCTTTTGAAGGCAAGAGCTCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 360  
 304 TTTTCTTTTGAAGGCAAGAGCTCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 363  
 361 CATGCTGTGAGAGCGGCGGCGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 420  
 364 CATGCTGTGAGAGCGGCGGCGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 423  
 421 GAGGCTGTGAGAGCGGCGGCGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 480  
 424 GAACTACTGGGGCTTAAGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 483  
 481 AGTGGCGGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 540  
 484 AAGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 543  
 541 GCGTCC 546  
 544 TCTTTT 549

## RESULT 9

US-08-985-526-37  
 ; Sequence 37, Application US/08985526  
 ; Patent No. 6080728  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mixson, James A  
 ; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA  
 ; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
 ; TITLE OF INVENTION: THERAPY  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: Connolly, Roy, Lodge, & Hurtz  
 ; STREET: 1220 Market Street, P.O. Box 2207  
 ; CITY: Wilmington  
 ; STATE: Delaware  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19899  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/985,526  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/608,845  
 ; FILING DATE: 16-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMorrow Jr., Robert G  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (302) 658-9141  
 ; TELEFAX: (302) 658-5613  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 565 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-985-526-37

Query Match 69.8%; Score 381.2; DB 3; Length 565;  
 Best Local Similarity 81.1%; Pred. No. 3.1e-76;  
 Matches 443; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

1 CACAGCCGCGGACCTTCCAGCCGGTGTCTCACTGTTGGGCTCAACAGCCCTCTGCA 60  
 11 CATCTCATCAGACTTTTACGACTGTCTCACTGTGTGGACACTGAACACCCCTGTCT 70  
 61 GGCAGCATGCGGGGCAATCGCGGGGCGCACTTCAGTGTCTCAAGCGCGGGCCGTG 120  
 71 GGAAGCATGCGGTGTATTCGTGTGAGAGATTTTCAGTGTCTTCAGCAAGCGCGGCGTG 130  
 121 GGGCTGGGGGCACTTTCGCGGCTTCTGTCTCTGCGGCTGTGAGAGACTGTACAGATC 180  
 124 GGGCTGTGGGCACTTTCGCGGCTTCTGTCTCTGTGAGAGACTGTACAGATC 183  
 181 GTGGCGGCTGTGAGAGCGGCGGCGGCTGTGAGAGACTGTACAGATC 240  
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 241 CCCAGCTGGAGGCTCTGTCTCAAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 300  
 244 CCCAGCTGGAGCTCTGTCTCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 303  
 301 TTCTCTTTTGAAGGCAAGAGCTCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 360  
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 361 CATGCTGTGAGAGCGGCGGCGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 420  
 364 CATGCTGTGAGAGCGGCGGCGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 423  
 421 GAGGCTGTGAGAGCGGCGGCGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 480  
 424 GAACTACTGGGGCTTAAGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 483  
 481 AGTGGCGGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCT 540  
 484 AAGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 543  
 541 GCGTCC 546  
 544 TCTTTT 549

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1 RESULT 10
2 US-09-561-500-12
3 ; Sequence 12, Application US/09561500
4 ; Patent No. 6342219
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Philip E. Thorpe
7 ; APPLICANT: Rolf A. Breken
8 ; TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
9 ; FILE REFERENCE: 4001.002500
10 ; CURRENT APPLICATION NUMBER: US/09/561,500
11 ; CURRENT FILING DATE: 2000-04-28
12 ; PRIOR APPLICATION NUMBER: 60/111,432
13 ; PRIOR FILING DATE: 1999-04-28
14 ; NUMBER OF SEQ ID NOS: 44
15 ; SOFTWARE: PatentIn Ver. 2.0
16 ; SEQ ID NO 12
17 ; LENGTH: 573
18 ; TYPE: DNA
19 ; ORGANISM: Artificial Sequence
20 ; FEATURE:
21 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
22 ; OTHER INFORMATION: OLIGONUCLEOTIDE
23 ; NAME/KEY: CDS
24 ; LOCATION: (1)..(573)
25 ; US-09-561-500-12

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Query Match	69.8%	Score	381.2	DB	4	Length	573
Best Local Similarity	81.1%	Pred.	3.2e-76				
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				Gaps			0
QY	1	CAAGACCAACCGGACCTTCAAGCCGAGTGTCTTCCACTGTGTGTCGCTCAACAGCCCCCTGTCA	60				
Db	22	CATATCATCATGAGGACTTTTCAAGCAGATGCTTCCACTGTGTGTCGCTCAACAGCCCCCTGTCT	81				
QY	61	GGGCGCATGCGGAGGACATCGCGGAGGCGGACCTTCAGTGTCTTCAAGAGAGGCGGGGCGGT	120				
Db	82	GGAGGCAATCGTGTATCCGTATGACAGCATTTTCATGTGTTCACGACACCCGAGACCTG	141				
QY	121	GGGCTGAGCGGACACTTCGCGGCTTCTCTGTCTTCGCGCTTCAGAGACCTGTACAGCATC	180				
Db	142	GGGCTGTGCGGACACTTCGCGGCTTCTCTGTCTTCAGGCTTCATATGATC	201				
QY	181	GTCGCGCGTGCAGACGCGGACGCGCTGTGCATGTCTAACCTTCAGAGACGTGTCTTT	240				
Db	202	GTCGCGCGTGCAGACGCGGAGTCTGTGTCCATGTCTAACCTTCAGAGACGTGTCTATCT	261				
QY	241	CCGAGCTGAGAGGCTCTGTTTCAAGGCTTCAGAGGTCGCGTGAAGCCCGGAGCAGCATC	300				
Db	262	CCGAGCTGAGACTCCCTGTTTCTGTGCTCCAGAGTCAATCTGACACCGGAGCCCGCATC	321				
QY	301	TTTCTCTTTGACGACAGAGACGTCTTGAGGACATCCCTGAGCCCAAGAGGCTGTG	360				
Db	322	TTTTCTTTTTCAGCGCAGAGATGTCTCTAAGACACCAAGCTTCGCGAGAGAGGTATG	381				
QY	361	CATGCTGTGACCCCAACGAGGCGACAGGCTACCGAGAGCTTATGTGACAGCGGCGAGG	420				
Db	382	CAGGCTGTGACCCCAAGGAGGAGGCTATGAGAGATTCTGTAGCATGTGGGATCT	441				
QY	421	GAGGCTCTTGTGACGAGGACTCTCTGTGTGAGGAGGAGGCTCTGTGTGAGGACG	480				

```

RESULT 11
US-09-561-108-12
; Sequence 12, Application US/09561108
; Patent No. 6342221
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/561,108
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; NAME/KEY: CDS
; LOCATION: (1)..(573)
; US-09-561-108-12

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	Query Match	86.8%;	Score 381.2;	DB 4;	Length 573;
	Best Local Similarity	81.1%;	Pred. No. 3,2e-76;		
	Matches 443;	Conservative 0;	Mismatches 103;	Indels 0;	Gaps 0
QY	1	CACAGCCACGCGACCTTCTCAGCCGCGTCTCACTCTGTTGGCTACACAGCCCCCTGTCA	60		
Db	22	CATACCTCATCGAGACTTTTTCAGCCAGGTCTCTCACTGTGGACATGAACCCCCCTGTCT	81		
QY	61	GGCGGCAATGCGGGGCAATCCGCGGGGCGGACCTTCAGTGTCTTCAGAGGCGGGGCGGTG	120		
Db	82	GGAGGCAATGCGGTGTATCCGTGAGACGATTTTCAGTGTCTTCAGAGGCGGGGCGGTG	141		
QY	121	GGGCTGGCGGGGCACTTTCGCGCCCTTCTCTCTCTGCGCTGCGACGTGACAGACTGTACAGATC	180		
Db	142	GGGCTGTGGGCGACCTTTCGCGGCTTTTCTGTCTTCAAGGTGCGAGGATCTATAGATC	201		
QY	181	GTGCGCGGTGCGCACGCGGCGACCGGTGCGCCATGTCATCTGAAGAGAGAGTGTGTTT	240		
Db	202	GTGCGCGGTGCGCACGCGGCGGTGTGTGCTCCATGTCAACTGTAAGAGAGAGTGTGTATCT	261		
QY	241	CCCAAGTGGAGAGCTGTCTTCTCAAGGCTCTGAAGGTTCGCTGAAGCCCGGGGCGACGATC	300		
Db	262	CCCAAGTGGAGACTCCCTGTTTTCTGTGCTCCAGGGGTCAACTGCACTCGGGGCCCGCATC	321		
QY	301	TTCCTCTTTGACGGCAAGAGAGTCTCTTAAGGCAACCCCACTTGGCCCCAAGAGGTGTGG	360		
Db	322	TTTTCTTTTGAACGACAGAAATGTCTTAAACACCCAGCTGGGCGCGAGAAAGGTATGG	381		
QY	361	CATGGCTCGAACCCCAACGGGCGGAGGCTTACCCGAGACTACTGTGAAGCTGGTCCGACG	420		
Db	382	CAGGGCTCGAACCCCAAGTGGGCGGAGGCTGATGAGAGATTACTGTGAACATGCGAAACT	441		
QY	421	GAGGCTCCTTGGCACGGGCGAGGCTCTGTGCTGTGGGGGCGAGGCTCTTGGGCGAG	480		
Db	442	GAACTCATGTGGGGCTACAGGTCAAGCTCTCTCCCTGCTGACAGCGAGGCTCTGTGAACAG	501		



QY	541	GCCTCC	546
Db	562	TCCTTC	567

```

RESULT 14
US-09-998-831-12
Sequence 12, Application US/09998831
Patent No. 6678941
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brecken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/561,108
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 573
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
NAME/KEY: CDS
LOCATION: (1)..(573)
US-09-998-831-12

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Query Match	69.8%;	Score 381.2;	DB 4;	Length 573;
Best Local Similarity	81.1%;	Pred. No. 3.2e-76;		
Matches 443;	Conservative	0;	Mismatches 103;	Indels 0;
				Gaps 0;

QY	1	AACGGCACCGGAACTTCCAGCCGCTGCCACTGGTTGGCTTCACACGCCCTGGCA	60
Db	22	CATCTCATCCAGAACTTTCCAGCAGTGTCCACTGGTGGCATGAACACCCCTGTCT	81
QY	61	GCGCGCATCGGGGGCATCCGCGGGGCGCACTTCCAGTCTTCAGCAGGCGCGGGCGTG	120
Db	82	GGAGGACATCGTGGTATCCGTGAGAGGAGATTTCCAGTGGCTTCAGCAAGGCCGAGCGTG	141
QY	121	GGGTGGGGGGAGACCTTTCGCGGCGTTTCCCTGCTCCCGGCTTCGAGAGCATGTACAGCATC	180
Db	142	GGGCTGTCCGGGACCTTTCGCGGCTTTTCTCTGCTCTTAGGGTCGAGGATCTCTATZMACATC	201
QY	181	GTGGGCGTGGCCAGCGCGCAGCCGTGCCATCGTCAACTCAGAGCAGACTGTGTTT	240
Db	202	GTGGGCGGTGTGACCGGGGGGTCTGAGCCCATCGTCAACTCAGAGCAGAGGTGTACTCT	261
QY	241	CCAGCGCTGGGAGGCTCTGTCTCCAGGCTCTGAGGTGTCGCGCTGAAGCCCGGGAGTACGCATC	300
Db	262	CCAGCTGGGACCTCTCTGTTTCTTGTGCTTCCAGGGTAACTGACATCCCGGGGCGCGATC	321
QY	301	TTCTCTTTGACGAGCAGAGACGTCTCTGAGGACCCCACTGGGCCCAAGAACCTGTGG	360
Db	322	TTTTCTTTTGAAGGACAGAGATGTCTTGAGACACCAGCCTGGCGCGAAGAACCTGATGG	381
QY	361	CATGGCTCGGAGCCCAACGAGCGGCGAGGCTGACCGGAGCTACTGTGAGACGTGGCGGAGG	420
Db	382	CACGGCTCGGAGCCCAAGTGGGCGGAGGCTGTGATGAGATTCTGTGAGAACATGGCAACT	441
QY	421	GAGGCTTCCTCGGACAGGGCCAGGCTTCTGCTGCTGTGGGGGCAAGCTCTCTGGGGGAG	480
Db	442	GAAACTACTGGGGCTACAGGTCAGGGCTCTCCCTGTGTACGGAGGCTCTTGAGACAG	501
QY	481	AGTGGCGGAGTGGCATCAGCTTACATGTGTCTGTGATTGAGAACACTTTCATGACT	540
Db	502	AAAGCTGCAGGTGCACAAACAGCTACATGCTCTGTGTGATTTGAGAAATACCTTTCATGACC	561

QY	541	GCCTCC	546
Db	562	TCTTTC	567

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RESULT 15
US-09-231-077D-5
; Sequence 5, Application US/09231077D
; Patent No. 6653098
; GENERAL INFORMATION:
; APPLICANT: Harding, E.I.
; APPLICANT: Violand, B.N.
; TITLE OF INVENTION: Method of producing mouse and human
; FILE REFERENCE: S03071-00-US
; CURRENT APPLICATION NUMBER: US/09/231,077D
; CURRENT FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/075,587
; PRIOR FILING DATE: 1998-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 620
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(620)
; OTHER INFORMATION: n = A,T,C or G
US-09-231-077D-5

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Query Match	69.8%	Score 381.2	DB 4	Length 620
Best Local Similarity	81.1%	Pred. No. 3.2e-76		
Matches 443; Conservative	0	Mismatches 103	Indels 0	Gaps 0

QY	1	CAAGAGCAACCGGACCTTCCAGAGCGGGTGTGCATCGTGTGTGGCGTCAAGACCCCGCTGCA	60
Db	15	CATATCTATCAAGAGCTTTAGCGCAAGTGTCTCAACTGTGGTGCATCTGAACACCCCTCTGTCT	74
QY	61	GAGCGCATACGGGGGCATACGCGGGGGCGAATTCAGTACTCTTCAGACGGACGCGGGCGGTG	120
Db	75	GAGAGCATACGTGGTATACCGTGTGAAGCAATTCGATGTCTTCAGACGAACCCGAGCCGTG	134
QY	121	GAGGCTGAGGGGCACCTTTCGCGACCTTCTGTCTGTGGCGCTTGAGAGACTGTACAGATC	180
Db	135	GAGGCTGTGGGCACCTTCGCGGCTTTCCTGTCTCTCAAGGCTGCAGGATCTCATAGATC	194
QY	181	GTCGCGCGTGGCGACCGCCAGCCGTCGCCATGTGCATACCTGAAGACAGAGTCGTGTTT	240
Db	195	GTCGCGCGTGGCGACCGGGGGTGTGTGTGCCATGTGCATCGAAGAGACAGAGTGTCTACTT	254
QY	241	CCGAGCTGGGAGGCTGTGTTCTCAGGCTCTGAAGGTGCGCTGAAGCCCGGGGCACGCATC	300
Db	255	CCGAGCTGGGACTCCCTGTTTCTGTGGCTCCCAAGGTCAACTGCAACCCGGGGCCGGATC	314
QY	301	TTCTCCCTTTGACGGCAAGAGACGTCTTGAAGACCCCAACTGSCCCCGAAGAGCGTGTGG	360
Db	315	TTTTTTTGTGACGGCAGAGATGTCTTGAGACCCGACTGGCCGCGAAGAGCGTATGG	374
QY	361	CATGCGCTGGACCCCAACGGGGCGCAGGCTCAACGAGAGCTACTGTGAGACGTGGCGGACG	420
Db	375	CAGGCGCTGGACCCCAAGTGGGGAGGGGTGATGAAGAGTACTGTGAGCAATGGGGAATC	434
QY	421	GAGGCTCCCTCGGACAGGGGCCAGGCTCCCTCGTGGGGGGCGAGCGCTCTGGGGGAG	480
Db	435	GAAACTACTGGGGGCTACAGGTGAGGCTCTCTCCCTGTGTGTAGGCGAGGCTCTGGAAAG	494
QY	481	AGTGGCGGAGCTGCATCAACGCTTAATGTGTCTGTGATTTAGGAACAGCTTCAATCACT	540
Db	495	AAAGCTGCGAAGTGTCCCAACAGCTACATGTGTGTGATTTAGGAATAGCTTATGACC	554
QY	541	GCCTCTC	546

Db 555 TCTTC 560

Search completed: September 15, 2004, 20:12:14  
Job time : 80 secs

(D/h/18 Sept)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 18:07:50 ; Search time 2452 Seconds  
(without alignments)  
6649.572 Million cell updates/sec

Title: US-10-042-347-4

Perfect score: 546  
Sequence: 1 cacagcacagcagcagcttcca.....acagctcatcagctcc 546

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba.\*  
2: em\_estbm.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_ivv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_pig.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	707	BE908201	BR908201 601500458
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3	546	100.0	881	CD105862	CD105862 AGENCOURT
4	546	100.0	4230	BC063833	BC063833 Homo sapi

5	519	95.1	944	13	B0659398	B0659398 AGENCOURT
6	508.6	92.2	929	13	B0672290	B0672290 AGENCOURT
7	504.2	92.3	703	13	B0615520	B0615520 UI-H-FGO-
8	495	90.7	682	9	AM089583	AM089583 x2d0f03.x
9	490	89.7	683	12	BM683067	BM683067 UI-E-FOI-
10	487.2	89.2	832	12	BG387051	BG387051 60245749
11	485.2	88.9	979	13	B0673186	B0673186 AGENCOURT
12	476	87.2	884	12	B161007	B161007 60286213
13	474.2	86.8	618	9	AV696242	AV696242 AV696242
14	469.4	86.0	1093	13	B0723254	B0723254 AGENCOURT
15	463	83.0	664	13	B0632049	B0632049 UI-H-FBI-
16	453	83.0	715	9	AU125614	AU125614 AU125614
17	451.4	82.7	947	13	B0556872	B0556872 AGENCOURT
18	450.6	82.5	745	10	AM243446	AM243446 xm95d11.x
19	445	81.5	639	12	BM989137	BM989137 UI-H-DTI-
20	443.4	81.2	634	13	B0772348	B0772348 UI-H-EZ1-
21	443.2	81.2	650	9	A1856615	A1856615 w14f01.x
22	440.8	80.7	660	10	AM192502	AM192502 x145e10.x
23	438.4	80.3	717	9	A1890773	A1890773 wm95f07.x
24	434.4	79.6	634	9	A1970297	A1970297 wr09c02.x
25	434	79.5	616	13	B0158380	B0158380 AGENCOURT
26	425	77.8	726	9	A1814791	A1814791 wk65h07.x
27	419.2	76.8	630	10	BE475568	BE475568 nae46e04.
28	418	76.6	645	10	BE621228	BE621228 601494176
29	417.4	76.4	808	9	AM080065	AM080065 xe48c06.x
30	412	75.5	605	12	BM998650	BM998650 UI-H-DTI-
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32	406.2	74.4	577	10	BE046311	BE046311 hnd45a12.x
33	403.8	74.0	603	10	AM439633	AM439633 hb76d01.x
34	394	72.2	680	9	AM090100	AM090100 xc91d03.x
35	392.8	71.9	921	13	BX453476	BX453476 BX453476
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37	388	71.1	575	10	BE114979	BE114979 hr72b09.x
38	387.4	71.0	504	14	CF789984	CF789984 867322 MA
39	386.4	70.8	396	9	AV691878	AV691878 AV691878
40	386.4	70.8	402	9	AV689623	AV689623 AV689623
41	384.8	70.5	675	5	AF163657	AF163657 wr64c10.x
42	381.2	69.8	843	10	BF385854	BF385854 602046021
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45	380.2	69.6	715	14	CB596713	CB596713 AGENCOURT

## ALIGNMENTS

RESULT 1  
LOCUS BE908201  
DEFINITION BE908201.1 GI:10402537  
ACCESSION BE908201  
VERSION BE908201  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS NIH-MGC  
TITLE NIH-MGC  
JOURNAL  
COMMENT  
1 (bases 1 to 707)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA library Preparation: Life Technologies, Inc.  
CDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: ILAM9704 row: d column: 16  
High quality sequence stop: 688.

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Location/Qualifiers

1..707

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3902175"

/tissue\_type="epithelioid carcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Nct1; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."

## ORIGIN

Query Match 100.0%; Score 546; DB 10; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-85;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCTCTGCA 60  
 DB 11 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCTCTGCA 70  
 QY 61 GCGGCGATGCGGGGCACTCCGCGGGGCGGCACTTCCAGCTTCCAGCGCGGGCGCTG 120  
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 QY 121 GGGCTGGCGGCACTTCCGCGCTTCTCTGCTGCGGCTGCGAGACCTGTAAAGCATC 180  
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 QY 181 GTGGCGCTGCGGCACTCCAGCGGCTGCTCCATGTCAACTCAAGAGACGCTGTTT 240  
 DB 191 GTGGCGCTGCGGCACTCCAGCGGCTGCTCCATGTCAACTCAAGAGACGCTGTTT 250  
 QY 241 CCAGCTGGAGGCTCTGTTCTCAAGCTCTGAAGGCTCGTGAAGCCCGGGCAAGCATC 300  
 DB 251 CCAGCTGGAGGCTCTGTTCTCAAGCTCTGAAGGCTCGTGAAGCCCGGGCAAGCATC 310  
 QY 301 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCACTCCAGCTGCGGCGGAGAGGCTGTG 360  
 DB 311 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCACTCCAGCTGCGGCGGAGAGGCTGTG 370  
 QY 361 CATGCTCTGCACTCCCAAGGCGGCAAGCTGACCTGAAGATCTGTGAAGCTGTGCGAG 420  
 DB 371 CATGCTCTGCACTCCCAAGGCGGCAAGCTGACCTGAAGATCTGTGAAGCTGTGCGAG 430  
 QY 421 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTCTGCGGCGAG 480  
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 QY 481 AGTGCCTGCACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 DB 491 AGTGCCTGCACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550  
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RESULT 2  
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 DEFINITION mRNA sequence.  
 ACCESSION BE906253  
 VERSION BE906253.1 GI:10399595  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 1 (bases 1 to 757)

## AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC

## JOURNAL

TITLE

COMMENT

cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Imcye Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/HLN at:  
<http://image.llnl.gov>  
 Plate: LL9709 row: 1 column: 09

## FEATURES

High quality sequence. Stop: 757.

## source

Location/Qualifiers

1..757

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3904208"

/tissue\_type="epithelioid carcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Nct1; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."

## ORIGIN

Query Match 100.0%; Score 546; DB 10; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-85;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCTCTGCA 60  
 DB 36 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCTCTGCA 95  
 QY 61 GCGGCGATGCGGGGCACTCCGCGGGGCGGCACTTCCAGCTTCCAGCGCGGGCGCTG 120  
 DB 96 GCGGCGATGCGGGGCACTCCGCGGGGCGGCACTTCCAGCTTCCAGCGCGGGCGCTG 155  
 QY 121 GGGCTGGCGGCACTTCCGCGCTTCTCTGCTGCGGCTGCGAGACCTGTAAAGCATC 180  
 DB 156 GGGCTGGCGGCACTTCCGCGCTTCTCTGCTGCGGCTGCGAGACCTGTAAAGCATC 215  
 QY 181 GTGGCGCTGCGGCACTCCAGCGGCTGCTCCATGTCAACTCAAGAGACGCTGTTT 240  
 DB 216 GTGGCGCTGCGGCACTCCAGCGGCTGCTCCATGTCAACTCAAGAGACGCTGTTT 275  
 QY 241 CCAGCTGGAGGCTCTGTTCTCAAGCTCTGAAGGCTCGTGAAGCCCGGGCAAGCATC 300  
 DB 276 CCAGCTGGAGGCTCTGTTCTCAAGCTCTGAAGGCTCGTGAAGCCCGGGCAAGCATC 335  
 QY 301 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCACTCCAGCTGCGGCGGAGAGGCTGTG 360  
 DB 336 TTCTCTTTGACGCGCAAGAGAGTCTGAGGCACTCCAGCTGCGGCGGAGAGGCTGTG 395  
 QY 361 CATGCTCTGCACTCCCAAGGCGGCAAGCTGACCTGAAGATCTGTGAAGCTGTGCGAG 420  
 DB 396 CATGCTCTGCACTCCCAAGGCGGCAAGCTGACCTGAAGATCTGTGAAGCTGTGCGAG 455  
 QY 421 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTCTGCGGCGAG 480  
 DB 456 GAGGCTCCCTCGGCGCAAGGCGCTCTGCTGCTGCGGGGCGAGGCTCTCTGCGGCGAG 515  
 QY 481 AGTGCCTGCACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 DB 516 AGTGCCTGCACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575  
 QY 541 GCTCTCC 546  
 DB 576 GCTCTCC 581

RESULT 3  
 CD105862 881 bp mRNA linear EST 15-MAY-2003  
 LOCUS CD105862  
 DEFINITION AGENCOURT 14021788 NIH MGC 179 Homo sapiens cDNA clone  
 IMAGE:30355831 5', mRNA sequence.  
 ACCESSION CD105862  
 VERSION CD105862.1 GI:30759036  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 881)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLM at:  
<http://image.llnl.gov>  
 Plate: NDMA424 row: 9 column: 24  
 High quality sequence stop: 689.

FEATURES  
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 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:30355831"  
 /tissue\_type="Pituitary"  
 /lab\_host="DH10B-Tcon A (T1 and T5 phage resistances)"  
 /clone\_lib="NIH MGC\_179"  
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV  
 (destroyed); Site 2: NotI; Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.1 kb. Library was  
 constructed by (Invitrogen). Note: this is a NIH\_MGC  
 Library."

## ORIGIN

Query Match 100.0%; Score 546; DB 14; Length 881;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-85;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCTGCTCA 60  
 292 CACAGCCACCGGCACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCTGCTCA 351  
 61 GCGGCGATGCGGGGCACTCCGCGGGCGGCACTTCCAGTGTTCAGCAGGGGCGGGCCTG 120  
 352 GCGGCGATGCGGGGCACTCCGCGGGCGGCACTTCCAGTGTTCAGCAGGGGCGGGCCTG 411  
 121 GGGCTGCGGGGCACTTCCGCGCTTCTGCTGCTGCGCGCTGCGAGACTGTACAGCATC 180  
 412 GGGCTGCGGGGCACTTCCGCGCTTCTGCTGCTGCGCGCTGCGAGACTGTACAGCATC 471  
 181 GTGCGCGGTGCGGCACTCCGCGCGGCTGCTGCTCAACCTTCAAGAGAGAGCTGCTGTT 240  
 472 GTGCGCGGTGCGGCACTCCGCGCGGCTGCTGCTCAACCTTCAAGAGAGAGCTGCTGTT 531  
 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCGGCACTC 300  
 532 CCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCGGCACTC 591  
 301 TTCTCTTTGACGGCAAGAGCTCTGAGGAGACCCCACTGGGCCCGAGAGAGAGCTGAGG 360  
 592 TTCTCTTTGACGGCAAGAGCTCTGAGGAGACCCCACTGGGCCCGAGAGAGAGCTGAGG 651

QY 361 CATGCTCGAACCACCCACCGGCGGCTGACCGAGAGCTACTGTGAGAGCTGCGGAGC 420  
 DB 652 CATGCTCGGACCCACCGGCGGCTGACCGAGAGCTACTGTGAGAGCTGCGGAGC 711  
 QY 421 GAGGCTCCCTGGGCGACGGGCGGCTCTGCTGCTGCGGGGAGGAGGCTCTGCGGCGAG 480  
 DB 712 GAGGCTCCCTGGGCGACGGGCGGCTCTGCTGCTGCGGGGAGGAGGCTCTGCGGCGAG 771  
 QY 481 AGTCCGCGAGCTGCTCATACGCTTACATCGTCTGCTGATTAAGAACAGCTTCACTACT 540  
 DB 772 AGTCCGCGAGCTGCTCATACGCTTACATCGTCTGCTGATTAAGAACAGCTTCACTACT 831  
 QY 541 GCCTCC 546  
 DB 832 GCCTCC 837

RESULT 4  
 BC063833 4230 bp mRNA linear HTC 09-DEC-2003  
 LOCUS BC063833  
 DEFINITION Homo sapiens cDNA clone IMAGE:6181818, containing frame-shift  
 errors.  
 ACCESSION BC063833  
 VERSION BC063833.1 GI:39645297  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 4230)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stepieton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Ubedin, T.B., Tosiyaki, S.,  
 Canninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultky, S.W.,  
 Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Hellon, E., Kettman, M., Madan, A., Young, A.C., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, D.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,  
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE  
 JOURNAL  
 PUBLISHED  
 REFERENCE  
 AUTHORS  
 JOURNAL  
 TITLE  
 JOURNAL

REMARK  
 COMMENT  
 NIH-MGC Project URL: <http://mgs.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@cgsc.bc.ca  
 Steven Jones, Jennifer Amano, Ian Bosdet, Yaron Butlerfield,  
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Leticia Hsiao, Martin Krzywinski, Beta Kutsche, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
 Nees, Pawan Pandey, Anna-Liisa Prabhu, Parveen Saeedi, Jacqueline

Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natsija van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18765747

## FEATURES

Location/Qualifiers  
1..4230  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6181818"  
/tissue\_type="Peripheral Nervous System, dorsal root ganglion"  
/clone\_id="Lupsk1\_dorsal\_root\_ganglion"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"

## ORIGIN

Query Match 100.0%; Score 546; DB 11; Length 4230;  
Best Local Similarity 100.0%; Pred. No. 1.5e-84;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACACGCCACCGGCACTTCCAGCGGTGTCCAGTGTGGCTTCAACACCCCTCTGCA 60  
|||  
3495 CACACGCCACCGGCACTTCCAGCGGTGTCCAGTGTGGCTTCAACACCCCTCTGCA 3554  
61 GCGCGCATGCGGGGCACTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 120  
|||  
3555 GCGCGCATGCGGGGCACTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 3614  
121 GCGCGCATGCGGGGCACTTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 180  
|||  
3615 GCGCGCATGCGGGGCACTTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 3674  
181 GCGCGCATGCGGGGCACTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 240  
|||  
3675 GCGCGCATGCGGGGCACTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 3734  
241 CCGAGCTGGAGAGCTGTTTCAAGGCTTGAAGGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 300  
|||  
3735 CCGAGCTGGAGAGCTGTTTCAAGGCTTGAAGGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 3794  
301 TTCTCTTTGACGCGCAAGGAGCTCTTGAAGGAGCCCACTTGGCCCCAAGAGAGCTGTGG 360  
|||  
3795 TTCTCTTTGACGCGCAAGGAGCTCTTGAAGGAGCCCACTTGGCCCCAAGAGAGCTGTGG 3854  
361 CATTGCTGGAGCCCGCAAGCGGGGCGAGCTGAACGAGAGCTATGAGAGAGCTGTGGAGAG 420  
|||  
3855 CATTGCTGGAGCCCGCAAGCGGGGCGAGCTGAACGAGAGCTATGAGAGAGCTGTGGAGAG 3914  
421 GAGGCTCCCTCGAGCGACGCGGCGAGGCTCTTCTGCTGCTGGGAGGCGAGGCTCTTGGAGG 480  
|||  
3915 GAGGCTCCCTCGAGCGACGCGGCGAGGCTCTTCTGCTGCTGGGAGGCGAGGCTCTTGGAGG 3974  
481 AGTGGCGGAGCTGCTCAATCAAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
|||  
3975 AGTGGCGGAGCTGCTCAATCAAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4034  
541 GCTGCC 546  
|||  
4035 GCTGCC 4040

RESULT 5  
BU859398/c 944 bp mRNA linear EST 16-OCT-2002  
LOCUS  
DEFINITION AGAGCGCTGAGCCCGCAAGCGGGGCGAGCTGAACGAGAGCTATGAGAGAGCTGTGGAGAG 293  
IMAGE:6650260 5', mRNA sequence.

ACCESSION BU859398  
VERSION BU859398.1 GI:24044390  
EST.

## KEYWORDS

## SOURCE

## ORGANISM

## Homo sapiens (human)

## Homo sapiens

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 944)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>  
Plate: LHC2895 row: d column: 04  
High quality sequence stop: 572.

## FEATURES

## source

1..944  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6650260"  
/tissue\_type="teratocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH MGC 109"

/note="Organ: ovary; Vector: pOT7; Site 1: EcoRI; Site 2: XhoI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

## ORIGIN

Query Match 95.1%; Score 519; DB 13; Length 944;  
Best Local Similarity 98.0%; Pred. No. 4.5e-80;  
Matches 536; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

1 CACACGCCACCGGCACTTCCAGCGGTGTCCAGTGTGGCTTCAACACCCCTCTGTC 59  
|||  
712 CAGGTGACCGGAGCTTCCAGCGGTGTCCAGTGTGGCTTCAACACCCCTCTGTC 653  
60 AGCGGCGCATGCGGGGCACTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 119  
|||  
652 AGCGGCGCATGCGGGGCACTCCGCGGGGCGAGCTTCCAGTGTGGCTTCAACAGCGCGGCGGTG 593  
120 GAGGCTGGGAGGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 179  
|||  
592 GAGGCTGGGAGGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533  
180 GAGGCTGGGAGGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239  
|||  
532 GAGGCTGGGAGGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 473  
240 TCCAGCTGGAGGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 299  
|||  
472 TCCAGCTGGAGGAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413  
300 CTCTCTCTTTGACGCGCAAGGAGCTCTTGAAGGAGCCCACTTGGCCCCAAGAGAGCTGTGG 359  
|||  
412 CTCTCTCTTTGACGCGCAAGGAGCTCTTGAAGGAGCCCACTTGGCCCCAAGAGAGCTGTGG 353  
360 GCATGCTGGAGCCCGCAAGCGGGGCGAGCTGAACGAGAGCTATGAGAGAGCTGTGGAGAG 419  
|||  
352 GCATGCTGGAGCCCGCAAGCGGGGCGAGCTGAACGAGAGCTATGAGAGAGCTGTGGAGAG 293





Coordinate Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA  
Tel.: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)).  
The following repetitive elements were found in this cDNA  
sequence: 1-44, >POLY A#simple\_repeat (matched complement)  
Seq primer: M13 Forward  
POLYA=yes.

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UT1-E-B01-a[d-g-02-0-UT1"  
 /tissue\_type="fetal eye"  
 /dev\_stage="fetal"  
 /lab\_host="DH10s (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UT1-E-B01"  
 /note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a  
 modified polyLinker; Site 1: EcoR I; Site 2: Not I;  
 UT-E-B01 is a normalized cDNA library containing the  
 following tissue(s): fetal eye. The library was  
 constructed according to Bonaldo, Lennom and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT773-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 GCGCATATAC. This library was created for the program,  
 Gene Discovery in the Visual System, supported by National Eye  
 Institute (NEI).  
 TAG\_TISSUE=human fetal eye  
 TAG\_LIB=UT1-E-B01  
 TAG\_SEQ=GCGCATATAC"

Query Match	89.7%	Score 490;	DB 12;	Length 683;
Best Local Similarity	99.8%;	Pred. No. 4.3e-75;		
Matches 490; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

FEATURES	RESULT 10	EST 12-MAR-2001
LOCUS	BG387051	
DEFINITION	BG387051	832 bp mRNA linear EST 12-MAR-2001
ACCESSION	G02455749F1 NIH_MGC_15	Homo sapiens cDNA clone IMAGE:4582933 5',
VERSION	BG387051	mRNA sequence.
KEYWORDS	BG387051.1	GI:13280497
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	1 (bases 1 to 832)	
JOURNAL	NIH-MGC <a href="http://mgs.nci.nih.gov/">http://mgs.nci.nih.gov/</a>	
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)	
	Contact: Robert Strausberg, Ph. D.	
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>	
	Tissue Procurement: ATCC	
	cDNA Library Preparation: Ling Hong/Rubin Laboratory	
	cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: NIH Intramural Sequencing Center	
	Clone distribution: MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LNL at:	
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>	
	Plate: LNCM306 row: a column: 14	
	High quality sequence stop: 679.	
	Location/Qualifiers	

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FEATURES
source
Location/Qualifiers
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/db_xref="Ena:9606"
/clone="IMAGE:582933"
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## ORIGIN

Query Match 89.2%; Score 487.2; DB 12; Length 832;  
 Best Local Similarity 97.9%; Pred. No. 1.4e-74;  
 Matches 525; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

/note="Organ: colon; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)";

1 CACAGCCACCGGACCTTCCAGCGGATGCTCCAGCTGGTGGCTCAACAGCCCTCTGTCA 60  
 214 CACAGCCACCGGACCTTCCAGCGGATGCTCCAGCTGGTGGCTCAACAGCCCTCTGTCA 273  
 61 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 120  
 274 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 333  
 121 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 180  
 334 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 393  
 181 GTCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 240  
 394 GTCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 453  
 241 CCGAGCTGGAGGCTCTGTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 300  
 454 CCGAGCTGGAGGCTCTGTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 513  
 301 TTCTCTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 514 TTCTCTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 573  
 361 CATGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 418  
 574 CATGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 633  
 419 CGAGGAGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 478  
 634 CGAGGAGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692  
 479 AGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 534  
 693 AGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 748

RESULT 11  
 B0673186 979 bp mRNA linear EST 15-JUL-2002  
 LOCUS AGENCOURT\_9414390 NIH\_MGC\_102 Homo sapiens cDNA clone IMAGE:6272287  
 DEFINITION 5', mRNA sequence.  
 B0673186  
 ACCESSION B0673186.1 GI:21784020  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 979)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation

## FEATURES

source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLC2450 row: g column: 08  
 High quality sequence stop: 638.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6272287"  
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 /clone\_id="NIH\_MGC\_102"  
 /note="Organ: salivary gland; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library.";

## ORIGIN

Query Match 88.9%; Score 485.2; DB 13; Length 979;  
 Best Local Similarity 97.6%; Pred. No. 3.2e-74;  
 Matches 535; Conservative 0; Mismatches 8; Indels 5; Gaps 4;

1 CACAGCCACCGGACCTTCCAGCGGATGCTCCAGCTGGTGGCTCAACAGCCCTCTGTCA 60  
 227 CACAGCCACCGGACCTTCCAGCGGATGCTCCAGCTGGTGGCTCAACAGCCCTCTGTCA 286  
 61 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 120  
 287 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 346  
 121 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 180  
 347 GGCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 406  
 181 GTCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 240  
 407 GTCAGGATGCGGAGCATCCGCGGAGCGGACCTTCCAGCTGGTGGCTCAACAGCGGAGCGTG 466  
 241 CCGAGCTGGAGGCTCTGTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 300  
 467 CCGAGCTGGAGGCTCTGTCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 526  
 301 TTCTCTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 527 TTCTCTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 586  
 361 CATGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 587 CATGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 646  
 421 GAGGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 478  
 647 GAGGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 706  
 479 AGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 535  
 707 AGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 766  
 536 TGAATGCC 543  
 767 TGAATGCC 774

RESULT 12  
 B1161007 884 bp mRNA linear EST 05-JUL-2001  
 LOCUS B1161007  
 DEFINITION 602865213f1 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:5019339 5',

ORIGIN

	Db	362	C96GCA098GGACAGCCTCCCTCGCTGTCGG666GCAAGCTCCTG666GACAATGCCGGA	421
Oy	491	GCTGCATTACAGCCTTACATGTGCTCTTGATTTAGAAGACTTATGATGCTCC	546	
Db	422	GCTGCATTACAGCCTTACATGTGCTCTTGATTTAGAAGACTTATGATGCTCC	477	
RESULT 13				
LOCUS	AV696242	618 bp	mRNA	linear EST 16-JAN-2002
DEFINITION	AV696242 KRC Homo sapiens CDNA clone GCEA602 5', mRNA sequence.			
ACCESSION	AV696242			
VERSION	AV696242.1	GI:10298105		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 618)			
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Gu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Pu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding nonaneous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 21655106			
TITLE	11752456			
JOURNAL	Contact: Zeguang Han			
MEDLINE	Chinese National Human Genome Center at Shanghai			
PUBMED	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel.: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.			
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	/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"			
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Best Local Similarity	92.9%; Pred. No. 2,3e-72;			
Matches	508; Conservative 0; Mismatches 38; Indels 1; Gaps 1;			
Oy	1	CACAGCACCGGAACTTCCAGCCGGTGTCCACCCTGATGCGCTCAAGAGCCCCCTGTCA	60	
Db	66	CACAGTACCCGAGACTTCCAGCCGGTGTCCACCCTGATGCGCTCAAGAGCCCCCTGTCA	125	
Oy	61	GGCGCATGGGGGATCCGGGGGGGCGCACTTCCAGAGTCTTCAGACGCGCGGCGCTG	120	
Db	126	GGCGCATGGGGGATCCGGGGGGGCGCACTTCCAGAGTCTTCAGAGCGCGGCGCTG	185	
Oy	121	GGGCTGGCGGAGCACTTCGCGCTTCTCTGCTCGGCGCTCGAGAC-CTGTAAGCAT	179	
Db	186	GGGCTGGCGGAGCACTTACCGGCTTCTCTGCTCGGCGCTCGAGACACTGTAAGCAT	245	
Oy	180	CGTGGCCGTGTCCACCGCGGACCGGTGCGCATGTCAACTCAAGACAGCTGCTGT	239	
Db	246	CGTGGCCGTGTCCACCGCGGACCGGTGCGCATGTCAACTCAAGACAGCTGCTGT	305	
Oy	240	TCCCACTGGAGAGCTCTGTTCAGAGGCTCTGAAGGTCGTAAGGCCGGGGCAGCAT	299	

Db 306 TCCACGCTGGAGAGCTCTGTTCTCAAGCTCTGAGGGTCCGCTGAAAGCCGAGGACCGAT 365  
 QY 300 CTTCTCTTTGACGAGAGAGCTCTGAGGACCCCACTGAGCCCAAGAGCTGTG 359  
 Db 366 CTTCTCTTTGACGAGAGAGAGCTCTGAGGACCCCACTGAGGACCCCAAGAGCTGTG 425  
 QY 360 GATGAGCTGGAG 419  
 Db 426 GATGAGCTGGAG 485  
 QY 420 GAGAGCTCTCTCGAG 479  
 Db 486 GAGAGCTCTCTCGAG 545  
 QY 480 GAGTCCGAG 539  
 Db 546 CATGCGGAG 605  
 QY 540 TGCCTCC 546  
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RESULT 14  
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 DEFINITION AGENCORT 8486770 lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
 ACCESSION B0723254  
 VERSION B0723254.1 GI:21862151  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 1093)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLNL13604 row: k column: 23  
 High quality sequence stop: 437.  
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 /lab\_host="DH10B"  
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 5'-TCGACCCACGAGTCG-3' and  
 5'-GACTAGTCTAGATCGAGCGCGCCCTT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by a life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."

ORIGIN

Query Match 86.0%; Score 469.4; DB 13; Length 1093;  
 Best Local Similarity 96.8%; Pred. No. 1.8e-71;  
 Matches 479; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
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 QY 104 AGCAGGCGGAGGAG 163  
 Db 61 AGCAGGCGGAGGAG 120  
 QY 164 AGGACTGTACAGATGTCGCGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223  
 Db 121 AGGACTGTACAGATGTCGCGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
 QY 224 AGGAG 283  
 Db 181 AGGAG 240  
 QY 284 AGCCCGGAG 343  
 Db 241 AGCCCGGAG 300  
 QY 344 CCAG 403  
 Db 301 CCAG 360  
 QY 404 GTGAG 463  
 Db 361 GTGAG 420  
 QY 464 GCAAGCTCTCTGAG 523  
 Db 421 GCAAGCTCTCTGAG 480  
 QY 524 AGAAG 538  
 Db 481 AGAAG 495

RESULT 15  
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 ACCESSION B0632049  
 VERSION B0632049.1 GI:22299304  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 664)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: James Martin  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@iowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 1-35, >AT-rich#low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
 Location/Qualifiers  
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/lab_host="DH10B (Life Technologies)"
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/note="Organ: Chondrosarcoma; Vector: pT73-Pac
(pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP FE1 is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
(dT)18 tail. The sequence tag for this library is
CGCTACGAGC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG TISSUE=human grade 2 chondrosarcoma cell line pool
TAG LIB=UT-H-FEI
TAG_SEQ=CGCTACGAGC"

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## ORIGIN

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Query Match      83.0%; Score 453; DB 13; Length 664;
Best Local Similarity 99.8%; Pred. No. 1,1e-68;
Matches 453; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 213 CGTCAACTCAAGGACAGGCTGTTCCTCAGCTGGAGGCTGTTCCTCAGGCTGA 272
DB 544 CGTCAACTCAAGGACAGGCTGTTCCTCAGCTGGAGGCTGTTCCTCAGGCTGA 485
QY 273 GGGTCGGCTGAAGCGCGGCGCAGATTTCTCTTGAACGCAAGGACGTCCTGAAGCA 332
DB 484 GGGTCGGCTGAAGCGCGGCGCAGATTTCTCTTGAACGCAAGGACGTCCTGAAGCA 425
QY 333 CCCCACTGGGCCCGAAGAGCGTGTGSCATGTGCAACCCCAACGGGCGAGGCTGAC 392
DB 424 CCCCACTGGGCCCGAAGAGCGTGTGSCATGTGCAACCCCAACGGGCGAGGCTGAC 365
QY 393 CGAGAGCTACTGTGAGACGTGCGGACGAGAGCTCCCTGGGCAACGGGCGAGGCTCTC 452
DB 364 CGAGAGCTACTGTGAGACGTGCGGACGAGAGCTCCCTGGGCAACGGGCGAGGCTCTC 305
QY 453 GGTGTGGGGGCGAGGCTCTTGGGCGAAGTGCAGAGCTGCGCATACGCTTACATCGT 512
DB 304 GGTGTGGGGGCGAGGCTCTTGGGCGAAGTGCAGAGCTGCGCATACGCTTACATCGT 245
QY 513 GCTTGCAATTGAGACAGCTTCATGACTGCTCC 546
DB 244 GCTTGCAATTGAGACAGCTTCATGACTGCTCC 211

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 Job time : 2457 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 19:29:47 ; Search time 355 Seconds

(without alignments)  
7738.624 Million cell updates/sec

Title: US-10-042-347-4

Sequence: 1 cagagccacgcgactcca.....acagctcatgactgcctcc 546

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 2: /cgn2\_6/prodata/2/pubna/PC1\_NEW\_PUB.seq:\*
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- 4: /cgn2\_6/prodata/2/pubna/US06\_PUBCOMB.seq:\*
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- 19: /cgn2\_6/prodata/2/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	546	US-10-042-347-4	Sequence 4, Appl1
2	546	100.0	549	US-10-135-872B-10	Sequence 10, Appl1
3	546	100.0	549	US-10-131-241-53	Sequence 53, Appl1
4	546	100.0	549	US-10-292-418-3	Sequence 3, Appl1
5	546	100.0	552	US-09-873-676-30	Sequence 30, Appl1
6	546	100.0	552	US-09-878-531-2	Sequence 2, Appl1
7	546	100.0	552	US-10-607-501-1	Sequence 1, Appl1
8	546	100.0	555	US-10-449-603-3	Sequence 3, Appl1
9	546	100.0	627	US-09-373-938-4	Sequence 4, Appl1
10	546	100.0	1158	US-10-449-609-5	Sequence 3, Appl1
11	546	100.0	3394	US-09-880-107-2178	Sequence 2178, Appl1
12	546	100.0	4551	US-10-060-036-144	Sequence 144, Appl1
13	546	100.0	4875	US-10-264-049-835	Sequence 835, Appl1
14	545	99.8	551	US-10-080-797-2	Sequence 2, Appl1

15	542.8	99.4	641	US-10-432-364-4	Sequence 4, Appl1
16	538	98.5	555	US-10-210-172-161	Sequence 161, Appl1
17	534	97.8	534	US-10-042-347-6	Sequence 6, Appl1
18	534	97.8	534	US-10-131-241-59	Sequence 59, Appl1
19	493.6	90.4	540	US-10-131-241-48	Sequence 48, Appl1
20	419.6	76.8	552	US-10-131-241-50	Sequence 50, Appl1
21	419.6	76.8	552	US-10-292-418-34	Sequence 34, Appl1
22	418	76.6	555	US-09-938-391-3	Sequence 3, Appl1
23	418	76.6	829	US-09-938-391-1	Sequence 1, Appl1
24	416.4	76.3	482	US-10-210-172-163	Sequence 163, Appl1
25	405.6	74.3	480	US-10-210-172-165	Sequence 165, Appl1
26	381.2	69.8	558	US-09-775-174-3	Sequence 3, Appl1
27	381.2	69.8	558	US-09-775-125-3	Sequence 3, Appl1
28	381.2	69.8	555	US-10-036-869-37	Sequence 37, Appl1
29	381.2	69.8	573	US-09-998-831-12	Sequence 12, Appl1
30	381.2	69.8	573	US-10-373-561-12	Sequence 12, Appl1
31	379.6	69.5	552	US-10-292-418-17	Sequence 17, Appl1
32	379.6	69.5	624	US-09-373-938-1	Sequence 1, Appl1
33	379.6	69.5	624	US-10-080-797-4	Sequence 4, Appl1
34	379.6	69.5	624	US-10-422-934-70	Sequence 70, Appl1
35	316.8	58.0	632	US-10-131-241-51	Sequence 51, Appl1
36	301.8	55.3	306	US-10-430-503-37	Sequence 37, Appl1
37	240	44.0	574	US-10-060-036-64	Sequence 64, Appl1
38	193.4	35.4	4077	US-10-087-192-1454	Sequence 1454, Appl1
39	176.8	32.4	5204	US-09-971-392-159	Sequence 159, Appl1
40	176.8	32.4	5222	US-10-133-937-67	Sequence 67, Appl1
41	176.8	32.4	5222	US-10-159-563-67	Sequence 67, Appl1
42	134.8	24.7	6048	US-10-433-793-32	Sequence 32, Appl1
43	123	22.5	900	US-10-131-241-45	Sequence 45, Appl1
44	111.2	20.4	6048	US-10-433-793-31	Sequence 31, Appl1
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#### ALIGNMENTS

RESULT 1  
US-10-042-347-4  
Sequence 4, Application US/10042347  
Publication No. US20030114370A1  
GENERAL INFORMATION:  
APPLICANT: Folkman, M. Judah  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Fragments  
FILE REFERENCE: 05213-0880 (43170-299874)  
CURRENT APPLICATION NUMBER: US/10/042,347  
CURRENT FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: US 09/315,689  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: US 60/106,343  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: US 09/154,302  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: US 08/740,168  
PRIOR FILING DATE: 1996-10-22  
PRIOR APPLICATION NUMBER: US 60/005,835  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: US 60/023,070  
PRIOR FILING DATE: 1996-08-02  
PRIOR APPLICATION NUMBER: US 60/026,263  
PRIOR FILING DATE: 1996-09-17  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 546  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-042-347-4  
Query Match 100.0%; Score 546; DB 15; Length 546;  
Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
Matches 546; Conservative 0; Mismatches 0; Gaps 0;

	Matches	546; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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QY	121	GGGCTGGGGGCACTTCCGCGCTTCTCTGCTCGCGCTCGAGGAACTGTAAAGATC	180						
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QY	361	CATGAGTCGGAACCCCAAGCGGCGAGGCTGACCGAAGACTACTGTGAGAGCTGCGGAGC	420						
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RESULT 3
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; Sequence 53, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; APPLICANT: Fortlier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
; TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-241-53

Query Match      100.0%; Score 546; DB 15; Length 549;
Best local Similarity 100.0%; Pred. No. 1,9e-13;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGCAGCATGCGGGGCACTCCGCGGGGCGCACTTCAGAGCTTTCAGAGCGGCGGCGGTG 120  
QY 121 GGCAGCATGCGGGGCACTTCGCGGCTTCTGTCTGTGCGCTTCAGAGCACTGTAGCATC 180  
DB 121 GGCAGCATGCGGGGCACTTCGCGGCTTCTGTCTGTGCGCTTCAGAGCACTGTAGCATC 180  
QY 181 GTGGCGCTGCGGAGCCGCGAGCGGCTTCATCTCACTCAAGGAGAGCTGTGTGTT 240  
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QY 421 GAGGCTCCCTCGGCGAGGCGGCGGAGGCTTCAGAGGCTTCAGAGCGGCGGCGGATC 480  
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QY 481 AGTGGCGGAGCTGCGATCAAGGCTTCAGAGGCTTCAGAGCGGCGGCGGATC 540  
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QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 4  
US-10-292-418-3

/ Sequence 3, Application US/10292418  
/ Publication No. US20030139365A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Li, Yue  
/ APPLICANT: Gillies, Stephen D  
/ TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as  
/ FILE REFERENCE: LEX-006C1  
/ CURRENT APPLICATION NUMBER: US/10/292,418  
/ PRIOR FILING DATE: 2002-11-12  
/ PRIOR APPLICATION NUMBER: 09/383,315  
/ PRIOR FILING DATE: 1999-08-25  
/ PRIOR APPLICATION NUMBER: US 60/097,883  
/ NUMBER OF SEQ ID NOS: 54  
/ SOFTWARE: Patent Ver. 2.0  
/ SEQ ID NO 3  
/ LENGTH: 549  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1)..(549)  
/ OTHER INFORMATION: endostatin  
US-10-292-418-3

Query Match 100.0%; Score 546; DB 15; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGAGCCACCGGACTTTCAGAGCGGCTCTCAACCTGTGGCTCAAGGCCCTCTGTCA 60  
DB 1 CAGAGCCACCGGACTTTCAGAGCGGCTCTCAACCTGTGGCTCAAGGCCCTCTGTCA 60  
QY 61 GGCAGCATGCGGGGCACTCCGCGGGGCGCACTTCAGAGCTTTCAGAGCGGCGGCGGTG 120  
DB 61 GGCAGCATGCGGGGCACTCCGCGGGGCGCACTTCAGAGCTTTCAGAGCGGCGGCGGTG 120  
QY 121 GGCAGCATGCGGGGCACTTCGCGGCTTCTGTCTGTGCGCTTCAGAGCACTGTAGCATC 180  
DB 121 GGCAGCATGCGGGGCACTTCGCGGCTTCTGTCTGTGCGCTTCAGAGCACTGTAGCATC 180  
QY 181 GTGGCGCTGCGGAGCCGCGAGCGGCTTCATCTCACTCAAGGAGAGCTGTGTGTT 240  
DB 181 GTGGCGCTGCGGAGCCGCGAGCGGCTTCATCTCACTCAAGGAGAGCTGTGTGTT 240  
QY 241 CCAGCTGGAGAGGCTGTCTCAAGGCTTCAGAGGCTTCAGAGCGGCGGCGGCGGATC 300  
DB 241 CCAGCTGGAGAGGCTGTCTCAAGGCTTCAGAGGCTTCAGAGCGGCGGCGGCGGATC 300  
QY 301 TTCTCTTTGACGAGCAAGGAGCTTCAGAGGCTTCAGAGCGGCGGCGGCGGATC 360  
DB 301 TTCTCTTTGACGAGCAAGGAGCTTCAGAGGCTTCAGAGCGGCGGCGGCGGATC 360  
QY 361 CATGCTCGGAGCCGCAAGGAGCTTCAGAGGCTTCAGAGCGGCGGCGGCGGATC 420  
DB 361 CATGCTCGGAGCCGCAAGGAGCTTCAGAGGCTTCAGAGCGGCGGCGGCGGATC 420  
QY 421 GAGGCTCCCTCGGCGAGGCGGCGGAGGCTTCAGAGGCTTCAGAGCGGCGGCGGATC 480  
DB 421 GAGGCTCCCTCGGCGAGGCGGCGGAGGCTTCAGAGGCTTCAGAGCGGCGGCGGATC 480  
QY 481 AGTGGCGGAGCTGCGATCAAGGCTTCAGAGGCTTCAGAGCGGCGGCGGATC 540  
DB 481 AGTGGCGGAGCTGCGATCAAGGCTTCAGAGGCTTCAGAGCGGCGGCGGATC 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 5  
US-09-873-676-30

/ Sequence 30, Application US/09873676  
/ Patent No. US20020077289A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Slim, Kim L.  
/ APPLICANT: MacDonald, Nicholas J.  
/ TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use  
/ FILE REFERENCE: 05213-0378 (43170-259333)  
/ CURRENT APPLICATION NUMBER: US/09/873,676  
/ PRIOR FILING DATE: 2001-06-04  
/ PRIOR APPLICATION NUMBER: US 60/209,065  
/ PRIOR FILING DATE: 2000-06-02  
/ PRIOR APPLICATION NUMBER: US 60/289,387  
/ PRIOR FILING DATE: 2001-05-08  
/ NUMBER OF SEQ ID NOS: 123  
/ SOFTWARE: Patent version 3.1  
/ SEQ ID NO 30  
/ LENGTH: 552  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-873-676-30

Query Match 100.0%; Score 546; DB 9; Length 552;  
Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	100.0%;	Score 546;	DB 13;	Length 552;
Best Local Similarity	100.0%;	Pred. No. 1,9e-132;		
Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

Qy	1	CAACACCACGCGACATTCCTCAGCCGGTCTCCACCTGTGTGGCTCAACAGCCCCCTGTCA	60
Db	1	CACACCCACCGCCACCTTCACGCGGTCTCCACCTGTGTGGCTCAACAGCCCCCTGTCA	60

  

Qy	61	GGCGGCATGGGGGGGCATCCGGGGGGCGACCTTCAGTGTCTTCCAGAGGCGGGCCCGTGG	120
Db	61	GGCGGCATGGGGGGGCATCCGGGGGGCGACCTTCAGTGTCTTCCAGAGGCGGGCCCGTGG	120

  

Qy	121	GGGCTGGTGGGGGACCTTCCTGGGCGCTTCCTGTGGCGCCGACAGGACCTGTAAAGATC	180
Db	121	GGGCTGGTGGGGGACCTTCCTGGGCGCTTCCTGTGGCGCCGACAGGACCTGTAAAGATC	180

Query Match	100.0 %;	Score 546;	DB 17;	Length 552;
Best Local Similarity	100.0 %;	Pred. No. 1.9e-132;		
Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	CACAGCACCGGACACTTCAGCCGGTGTCCACCTGGTTGGCTCAACACGCCCTCTGCA	60	
Db	1	CACAGCACCGGACACTTCAGCCGGTGTCCACCTGGTTGGCTCAACACGCCCTCTGCA	60	
Qy	61	GGCGGCATGCGGAGGCAATCGCGGGGCGACATTCAGTGTCTTCAGCAGGGCGCGGGCTGTG	120	
Db	61	GGCGGCATGCGGAGGCAATCGCGGGGCGACATTCAGTGTCTTCAGCAGGGCGCGGGCTGTG	120	
Qy	121	GGGCTGGCGGGGACATTCCTCCGCTCTTCTGTGCTCCGCGCGTGCAGAGACCTGTACACGATC	180	
Db	121	GGGCTGGCGGGGACATTCCTCCGCTCTTCTGTGCTCCGCGCGTGCAGAGACCTGTACACGATC	180	
Qy	181	GTGGCGCGGAGCGACCGGGCGAGCGGTGCCCATCTGTCAACTCAAGAGACGAGCTGTGTTT	240	
Db	181	GTGGCGCGGAGCGACCGGGCGAGCGGTGCCCATCTGTCAACTCAAGAGAGAGGCTGTGTTT	240	
Qy	241	CCGAGCTGGAGAGCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCTCCGGAGCACGCAATC	300	
Db	241	CCGAGCTGGAGAGGCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCTCCGGAGCACGCAATC	300	

QY 301 TTCTCTTTGACGCGCAAGAGAGCTCTGAGGCAACCCACCTGGCCCCCAAGAGCGTGTGG 360  
 Db 301 TTCTCTTTGACGCGCAAGAGAGCTCTGAGGCAACCCACCTGGCCCCCAAGAGCGTGTGG 360  
 QY 361 CATGGCTCGGACCCCAACGCGGCGAGGCTGACCCGAGAGCTTACTGTGAGACGTGGGAGAG 420  
 Db 361 CATGGCTCGGACCCCAACGCGGCGAGGCTGACCCGAGAGCTTACTGTGAGACGTGGGAGAG 420  
 QY 421 GAGGCTCTCCGCGCCCAACGCGGCGAGGCTCTCTGCTGCTGGGAGGCAAGGCTCTCGGAGAG 480  
 Db 421 GAGGCTCTCCGCGCCCAACGCGGCGAGGCTCTCTGCTGCTGGGAGGCAAGGCTCTCGGAGAG 480  
 QY 481 AGTCCGCGAGCTGCGCATCAGGCTTACATCGTGTCTGCTGATTTAGAAAGCTTTATGACT 540  
 Db 481 AGTCCGCGAGCTGCGCATCAGGCTTACATCGTGTCTGCTGATTTAGAAAGCTTTATGACT 540  
 QY 541 GCCTCC 546  
 Db 541 GCCTCC 546

## RESULT 8

US-10-449-609-3  
 ; Sequence 3, Application US/10449609  
 ; Publication No. US20040127407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHEN, WEN Y  
 ; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR  
 ; FILE REFERENCE: 035879-0163  
 ; CURRENT APPLICATION NUMBER: US/10/449,609  
 ; PRIOR FILING DATE: 2003-09-26  
 ; PRIOR APPLICATION NUMBER: 60/384,121  
 ; PRIOR FILING DATE: 2002-05-31  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 555  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-449-609-3

Query Match 100.0%; Score 546; DB 17; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAACAGCCCTCTGCA 60  
 Db 4 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAACAGCCCTCTGCA 63  
 QY 61 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCAGAGTCTTCCAGAGCGGCGCGTGG 120  
 Db 64 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCAGAGTCTTCCAGAGCGGCGCGTGG 123  
 QY 121 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGGACTTGTACAGATC 180  
 Db 124 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGGACTTGTGTGTG 183  
 QY 181 GTGGCGCGTCCGACCGCGGCGAGCCGTCGCCATGTCACCTCAAGAGACAGAGTGTGTGT 240  
 Db 184 GTGGCGCGTCCGACCGCGGCGAGCCGTCGCCATGTCACCTCAAGAGACAGAGTGTGTGT 243  
 QY 241 CCGAGCTGGGAGGCTGTGTTCTCAGGCTCTGAGGAGTCCGCTGAGAGCCCGGCGGCAAGATC 300  
 Db 244 CCGAGCTGGGAGGCTGTGTTCTCAGGCTCTGAGGAGTCCGCTGAGAGCCCGGCGGCAAGATC 303  
 QY 301 TTCTCTTTGACGCGCAAGAGAGTCTGAGAGCAACCCACCTGGCCCCCAAGAGCGTGTGG 360  
 Db 304 TTCTCTTTGACGCGCAAGAGAGTCTGAGAGCAACCCACCTGGCCCCCAAGAGCGTGTGG 363  
 QY 361 CATGGCTCGGACCCCAACGCGGCGAGGCTGACCCGAGAGCTTACTGTGAGACGTGGGAGAG 420

Db 364 CATGGCTCGGACCCCAACGCGGCGAGGCTGACCCGAGAGCTTACTGTGAGACGTGGGAGAG 423  
 QY 421 GAGGCTCTCCGCGCCCAACGCGGCGAGGCTCTCTGCTGCTGGGAGGCAAGGCTCTCGGAGAG 480  
 Db 424 GAGGCTCTCCGCGCCCAACGCGGCGAGGCTCTCTGCTGCTGGGAGGCAAGGCTCTCGGAGAG 483  
 QY 481 AGTCCGCGAGCTGCGCATCAGGCTTACATCGTGTCTGCTGATTTAGAAAGCTTTATGACT 540  
 Db 484 AGTCCGCGAGCTGCGCATCAGGCTTACATCGTGTCTGCTGATTTAGAAAGCTTTATGACT 543  
 QY 541 GCCTCC 546  
 Db 544 GCCTCC 549

## RESULT 9

US-09-373-938-4  
 ; Sequence 4, Application US/09373938  
 ; Publication No. US20020115202A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hallenbeck, Paul  
 ; APPLICANT: Chen, Cheayun Theresa  
 ; TITLE OF INVENTION: ADENOVIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC INHIBITORS  
 ; FILE REFERENCE: 4-308999P1  
 ; CURRENT APPLICATION NUMBER: US/09/373,938  
 ; PRIOR FILING DATE: 1999-08-13  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 627  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(627)  
 ; OTHER INFORMATION:  
 US-09-373-938-4

Query Match 100.0%; Score 546; DB 13; Length 627;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAACAGCCCTCTGCA 60  
 Db 76 CACAGCCACCGGCACTTCCAGCCGAGTCTCACTGAGTGGGCTCAACAGCCCTCTGCA 135  
 QY 61 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCAGAGTCTTCCAGAGCGGCGCGTGG 120  
 Db 136 GCGGCAATGCGGCGCATCCGCGGCGGCGGACTTCAGAGTCTTCCAGAGCGGCGCGTGG 195  
 QY 121 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGGACTTGTACAGATC 180  
 Db 196 GGGCTGGGCGGCACTTCCGCGGCTTCTGCTCTGCGCCCTGCGAGGACTTGTGTGTG 255  
 QY 181 GTGGCGCGTCCGACCGCGGCGAGCCGTCGCCATGTCACCTCAAGAGACAGAGTGTGTGT 240  
 Db 256 GTGGCGCGTCCGACCGCGGCGAGCCGTCGCCATGTCACCTCAAGAGACAGAGTGTGTGT 315  
 QY 241 CCGAGCTGGGAGGCTGTGTTCTCAGGCTCTGAGGAGTCCGCTGAGAGCCCGGCGGCAAGATC 300  
 Db 316 CCGAGCTGGGAGGCTGTGTTCTCAGGCTCTGAGGAGTCCGCTGAGAGCCCGGCGGCAAGATC 375  
 QY 301 TTCTCTTTGACGCGCAAGAGAGTCTGAGAGCAACCCACCTGGCCCCCAAGAGCGTGTGG 360  
 Db 376 TTCTCTTTGACGCGCAAGAGAGTCTGAGAGCAACCCACCTGGCCCCCAAGAGCGTGTGG 435  
 QY 361 CATGGCTCGGACCCCAACGCGGCGAGGCTGACCCGAGAGCTTACTGTGAGACGTGGGAGAG 420  
 Db 436 CATGGCTCGGACCCCAACGCGGCGAGGCTGACCCGAGAGCTTACTGTGAGACGTGGGAGAG 495  
 QY 421 GAGGCTCTCCGCGCCCAACGCGGCGAGGCTCTCTGCTGCTGGGAGGCAAGGCTCTCGGAGAG 480  
 Db 496 GAGGCTCTCCGCGCCCAACGCGGCGAGGCTCTCTGCTGCTGGGAGGCAAGGCTCTCGGAGAG 555

QY 481 AGTGGCCGAGCTGCTCATCGCTTACATGCTCTTCTGATGAGAGAGCTTCAACT 540  
|||||  
Db 556 AGTGGCCGAGCTGCTCATCGCTTACATGCTCTTCTGATGAGAGAGCTTCAACT 615  
QY 541 GCCTCC 546  
|||||  
Db 616 GCCTCC 621

## RESULT 10

US-10-449-609-5  
; Sequence 5, Application US/10449609  
; Publication No. US20040127407A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, MEN Y  
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR  
; FILE REFERENCE: 035879-0163  
; CURRENT APPLICATION NUMBER: US/10/449,609  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/384,121  
; PRIOR FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1158  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: hPRL\_G129R-Endostatin Fusion nucleotide sequence  
US-10-449-609-5

Query Match 100.0%; Score 546; DB 17; Length 1158;  
Best Local Similarity 100.0%; Pred. No. 1.8e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGCTCTCACTGCTTGGCTTCAAGCCCTGCTCA 60  
Db 607 CACAGCCACCGGACCTTCCAGCCGCTCTCACTGCTTGGCTTCAAGCCCTGCTCA 666  
QY 61 GGGGGCATGGGGGATCGGGGGGCGACCTTCCAGGCTTCCAGAGCCGAGCCGCTG 120  
Db 667 GGGGGCATGGGGGATCGGGGGGCGACCTTCCAGGCTTCCAGAGCCGAGCCGCTG 726  
QY 121 GGGGTGGGGGACCTTCCGCGCTTCTGCTCTGCTGCGCTGAGAGACTTGTACAGATC 180  
Db 727 GGGGTGGGGGACCTTCCGCGCTTCTGCTCTGCTGCGCTGAGAGACTTGTACAGATC 786  
QY 181 GTGGCCGCTGCGACCGCGCGACCGCTGCTCTCACTTCAAGAGAGAGCTGCTGTT 240  
Db 787 GTGGCCGCTGCGACCGCGCGACCGCTGCTCTCACTTCAAGAGAGAGCTGCTGTT 846  
QY 241 CCCAGCTGGAGAGCTGCTTCTCAAGGCTGAGAGGTCGAGTGAAGCCGAGGCAAGCATC 300  
Db 847 CCCAGCTGGAGAGCTGCTTCTCAAGGCTGAGAGGTCGAGTGAAGCCGAGGCAAGCATC 906  
QY 301 TTCTCTTTTGAAGGAGAGAGCTTCTGAGAGCAAGCCCACTTGGCCCAAGAGAGCTGTG 360  
Db 907 TTCTCTTTTGAAGGAGAGAGCTTCTGAGAGCAAGCCCACTTGGCCCAAGAGAGCTGTG 966  
QY 361 CATGCTCTGAGACCCCAACGGGCGAGGCTGAGACCGAGAGCTTCTGAGAGAGCTGTG 420  
Db 967 CATGCTCTGAGACCCCAACGGGCGAGGCTGAGACCGAGAGCTTCTGAGAGAGCTGTG 1026  
QY 421 GAGGCTCTCTGAGCGACAGGCGCGAGGCTCTGAGAGAGCTGAGAGAGCTGTGAGAG 480  
Db 1027 GAGGCTCTCTGAGCGACAGGCGCGAGGCTCTGAGAGAGCTGAGAGAGCTGTGAGAG 1086  
QY 481 AGTGGCCGAGCTGCTCATCGCTTACATGCTCTTCTGATGAGAGAGCTTCAACT 540  
Db 1087 AGTGGCCGAGCTGCTCATCGCTTACATGCTCTTCTGATGAGAGAGCTTCAACT 1146

QY 541 GCCTCC 546  
|||||  
Db 1147 GCCTCC 1152

## RESULT 11

US-09-880-107-2178  
; Sequence 2178, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Voekley, Joseph G.  
; APPLICANT: Scherf, Iwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2178  
; LENGTH: 3394  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548  
US-09-880-107-2178

Query Match 100.0%; Score 546; DB 9; Length 3394;  
Best Local Similarity 100.0%; Pred. No. 1.6e-132;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCCGCTCTCACTGCTTGGCTTCAAGCCCTGCTCA 60  
Db 1504 CACAGCCACCGGACCTTCCAGCCGCTCTCACTGCTTGGCTTCAAGCCCTGCTCA 1563  
QY 61 GGGGGCATGGGGGATCGGGGGGCGACCTTCCAGGCTTCCAGAGCCGAGCCGCTG 120  
Db 1564 GGGGGCATGGGGGATCGGGGGGCGACCTTCCAGGCTTCCAGAGCCGAGCCGCTG 1623  
QY 121 GGGGTGGGGGACCTTCCGCGCTTCTGCTCTGCTGCGCTGAGAGACTTGTACAGATC 180  
Db 1624 GGGGTGGGGGACCTTCCGCGCTTCTGCTCTGCTGCGCTGAGAGACTTGTACAGATC 1683  
QY 181 GTGGCCGCTGCGACCGCGCGACCGCTGCTCTCACTTCAAGAGAGAGCTGCTGTT 240  
Db 1684 GTGGCCGCTGCGACCGCGCGACCGCTGCTCTCACTTCAAGAGAGAGCTGCTGTT 1743  
QY 241 CCCAGCTGGAGAGCTGCTTCTCAAGGCTGAGAGGTCGAGTGAAGCCGAGGCAAGCATC 300  
Db 1744 CCCAGCTGGAGAGCTGCTTCTCAAGGCTGAGAGGTCGAGTGAAGCCGAGGCAAGCATC 1803  
QY 301 TTCTCTTTTGAAGGAGAGAGCTTCTGAGAGCAAGCCCACTTGGCCCAAGAGAGCTGTG 360  
Db 1804 TTCTCTTTTGAAGGAGAGAGCTTCTGAGAGCAAGCCCACTTGGCCCAAGAGAGCTGTG 1863  
QY 361 CATGCTCTGAGACCCCAACGGGCGAGGCTGAGACCGAGAGCTTCTGAGAGAGCTGTG 420  
Db 1864 CATGCTCTGAGACCCCAACGGGCGAGGCTGAGACCGAGAGCTTCTGAGAGAGCTGTG 1923  
QY 421 GAGGCTCTCTGAGCGACAGGCGCGAGGCTCTGAGAGAGCTGAGAGAGCTGTGAGAG 480  
Db 1924 GAGGCTCTCTGAGCGACAGGCGCGAGGCTCTGAGAGAGCTGAGAGAGCTGTGAGAG 1983  
QY 481 AGTGGCCGAGCTGCTCATCGCTTACATGCTCTTCTGATGAGAGAGCTTCAACT 540  
Db 1984 AGTGGCCGAGCTGCTCATCGCTTACATGCTCTTCTGATGAGAGAGCTTCAACT 2043

QY 541 GCCTCC 546  
 Db 2044 GCCTCC 2049

RESULT 12

US-10-060-036-144  
 ; Sequence 144, Application US/10060036  
 ; Publication No. US20030073144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benson, Darin R.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Lodes, Michael J.  
 ; APPLICANT: Persing, David H.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Jiang, Yugu  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.566  
 ; CURRENT APPLICATION NUMBER: US/10/060,036  
 ; NUMBER OF SEQ ID NOS: 4560  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 144  
 ; LENGTH: 4551  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-060-036-144

Query Match 100.0%; Score 546; DB 15; Length 4551;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 60  
 Db 4000 CACAGCCACCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 4059  
 QY 61 GGGGCGATGCGGGGATCCGGGCGGAGCTTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 120  
 Db 4060 GGGGCGATGCGGGGATCCGGGCGGAGCTTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 4119  
 QY 121 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 180  
 Db 4120 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 4179  
 QY 181 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 240  
 Db 4180 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 4239  
 QY 241 CCCAGCTGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 300  
 Db 4240 CCCAGCTGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 4299  
 QY 301 TTCTCTTTGAGCGGAGGAGCTCTGAGGAGCCCACTGCGGCGGAGGAGGAGCTGAG 360  
 Db 4300 TTCTCTTTGAGCGGAGGAGCTCTGAGGAGCCCACTGCGGCGGAGGAGGAGCTGAG 4359  
 QY 361 CATGCTGCGAGCCCAAGCGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 420  
 Db 4360 CATGCTGCGAGCCCAAGCGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 4419  
 QY 421 GAGGCTCCCTGCGGAGGAGGAGCTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 480  
 Db 4420 GAGGCTCCCTGCGGAGGAGGAGCTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 4479  
 QY 481 AGTGCGGAGCTGCGATCAAGCTTACATGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 540  
 Db 4480 AGTGCGGAGCTGCGATCAAGCTTACATGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 4539  
 QY 541 GCCTCC 546  
 Db 4540 GCCTCC 4545

RESULT 13

US-10-264-049-835  
 ; Sequence 835, Application US/10264049  
 ; Publication No. US20040005579A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Birse et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PA133PI  
 ; CURRENT APPLICATION NUMBER: US/10/264,049  
 ; CURRENT FILING DATE: 2002-10-04  
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569  
 ; PRIOR FILING DATE: 2001-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/209,467  
 ; PRIOR FILING DATE: 2000-06-07  
 ; NUMBER OF SEQ ID NOS: 4360  
 ; SOFTWARE: PatentIn Ver. 3.1  
 ; SEQ ID NO 835  
 ; LENGTH: 4875  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-264-049-835

Query Match 100.0%; Score 546; DB 16; Length 4875;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-132;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 60  
 Db 2512 CACAGCCACCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 2571  
 QY 61 GGGGCGATGCGGGGATCCGGGCGGAGCTTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 120  
 Db 2572 GGGGCGATGCGGGGATCCGGGCGGAGCTTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 2631  
 QY 121 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 180  
 Db 2632 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 2691  
 QY 181 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 240  
 Db 2692 GGGGCGGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 2751  
 QY 241 CCCAGCTGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 300  
 Db 2752 CCCAGCTGCGGAGCTTCCAGCCGGTCTCCAGCTGTTGCGCTCAACAGCCCTCTGCA 2811  
 QY 301 TTCTCTTTGAGCGGAGGAGCTCTGAGGAGCCCACTGCGGCGGAGGAGGAGCTGAG 360  
 Db 2812 TTCTCTTTGAGCGGAGGAGCTCTGAGGAGCCCACTGCGGCGGAGGAGGAGCTGAG 2871  
 QY 361 CATGCTGCGAGCCCAAGCGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 420  
 Db 2872 CATGCTGCGAGCCCAAGCGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 2931  
 QY 421 GAGGCTCCCTGCGGAGGAGGAGCTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 480  
 Db 2932 GAGGCTCCCTGCGGAGGAGGAGCTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 2991  
 QY 481 AGTGCGGAGCTGCGATCAAGCTTACATGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 540  
 Db 2992 AGTGCGGAGCTGCGATCAAGCTTACATGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 3051  
 QY 541 GCCTCC 546  
 Db 3052 GCCTCC 3057

RESULT 14

US-10-080-797-2  
 ; Sequence 2, Application US/10080797  
 ; Publication No. US20020181253A1  
 ; GENERAL INFORMATION:

```

1  APPLICANT: Camprochiaro, Peter A.
2  APPLICANT: Dixon, Katharine H.
3  APPLICANT: Brazzell, Romulus K.
4  TITLE OF INVENTION: METHOD FOR TREATING OCULAR
5  TITLE OF INVENTION: NEOVASCULARIZATION
6  FILE REFERENCE: 4-31881A
7  CURRENT APPLICATION NUMBER: US/10/080,797
8  CURRENT FILING DATE: 2002-02-21
9  NUMBER OF SEQ ID NOS: 21
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO 2
12     LENGTH: 551
13     TYPE: DNA
14     ORGANISM: Human
15 US-10-080-797-2

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Query Match          99.8%; Score 545; DB 14; Length 551;
Best Local Similarity 100.0%; Pred. No. 3.4e-13;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	2	ACAGCCACCGGCACTTCACACGGAGCTCCACCTGGATCGCCTTAAACATCCTCCCTGAC	361
Db	1	ACAGCCACCGGCACTTCACACGGAGCTCCACCTGGATCGCCTTAAACATCCTCCCTGAC	60
QY	62	GCGCATATCGGGGCAATCCGGGGGCGACATCCAAATGAGCTTCACACAGGGGGGGGGCGAG	121
Db	61	GCGCATATCGGGGCAATCCGGGGGCGACATCCAAATGAGCTTCACACAGGGGGGGGGCGAG	120
QY	122	GGCGAGGGGCACTTCGAGCGCTTCCTGCTCGGGCTGCAGACTTGACACTGACATCG	181
Db	121	GGCGAGGGGCACTTCGAGCGCTTCCTGCTCGGGCTGCAGACTTGACACTGACATCG	180
QY	182	TGCGCGCTGCACCGCGGCGACGCGTGGCCATCGTCAACTCAAGACGAGCTGCTGTTTC	241
Db	181	TGCGCGCTGCACCGCGGCGACGCGTGGCCATCGTCAACTCAAGACGAGCTGCTGTTTC	240
QY	242	CCAGCTGGAGAGCTCTGTTCTCAAGCTCTGAGGGGTCCGCTGAAGCCCGGGGGGAGCAATC	301
Db	241	CCAGCTGGAGAGCTCTGTTCTCAAGCTCTGAGGGGTCCGCTGAAGCCCGGGGGGAGCAATC	300
QY	302	TCTCTCTTGAACGGCAAGACGTCCTGAGGCAACCCACCTGGGCCCAAGAGAGCGTGTGGC	361
Db	301	TCTCTCTTGAACGGCAAGACGTCCTGAGGCAACCCACCTGGGCCCAAGAGAGCGTGTGGC	360
QY	362	ATTGCTGTGAAACCCAAACGGGCGAGGCTTGACCGGAGACTACTGTGAGACGTGTGCGAGCG	421
Db	361	ATTGCTGTGAAACCCAAACGGGCGAGGCTTGACCGGAGACTACTGTGAGACGTGTGCGAGCG	420
QY	422	AGGCTCTCTTGCGCAACGGGCGAGGCTCTCTGCTGTGGGGGGGCAAGCTCTTGGGGCA	481
Db	421	AGGCTCTCTTGCGCAACGGGCGAGGCTCTCTGCTGTGGGGGGGCAAGCTCTTGGGGCA	480
QY	482	GTGCGCGAGCTGCCATACGCTTAATGTGTCTCTGCAATGAGACAGGTCATGACAG	541
Db	481	GTGCGCGAGCTGCCATACGCTTAATGTGTCTCTGCAATGAGACAGGTCATGACAG	540
QY	542	CCTCC	546
Db	541	CCTCC	545

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RESULT 15
US-10-432-364-4
; Sequence 4, Application US/10/432364
; Publication No. US20040091996A1
; GENERAL INFORMATION:
; APPLICANT: VINGENE BIOTECHNOLOGY LIMITED
; TITLE OF INVENTION: A VIRUS WHICH CAN EXPRESS TUMOR ANGIOSTATIN FACTOR WITH HIGH EFFICIENCY
; TITLE OF INVENTION: SPECIFIC TUMOR CELLS AND THE USE OF IT
; FILE REFERENCE: jec010042pct
; CURRENT APPLICATION NUMBER: US/10/432,364
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 36

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: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 641
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: The nucleotide sequence of the recovered fragments from PCR amplification of the human endostatin gene after being digested with EcoRI and
: OTHER INFORMATION: inserted into vector pBluescript IKS(+) (ATCC, USA)
US-10-432-364-4

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Query Match	99.4%	Score 542.8;	DB 17;	Length 641;
Best Local Similarity	99.6%;	Pred. No. 1.2e-131;		
Matches 544; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	CCAGCCACCGGACATCTTCACGTCGATCTCCACCTGGTTCCTCAACTGGTTGGCGCTCAACAGCCCTCTGCA	60
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QY	61	GGCGGACATCGGAGGACATCCGCGGGGCGGACCTTCAGTGTCTCCAGCAGGCGCGGGGCGGTG	120
Db	142	GGCGGACATCGGAGGACATCCGCGGGGCGGACCTTCAGTGTCTCCAGCAGGCGCGGGGCGGTG	201
QY	121	GGGCTGGCGGGACCTTCCGGGCGCTTCCTGTCCTGTCGCGCTTCGCGCTTCGAGACCTGTACAGCATC	180
Db	202	GGGCTGGCGGGACCTTCCGGGCGCTTCCTGTCCTGTCGCGCTTCGAGACCTGTACAGCATC	261
QY	181	GGGCGCGGTTCGACGCGGCGACGCGTCCCATGTGTCACTTCAAGACGAGCTGTCTTT	240
Db	262	GGGCGCGGTTCGACGCGGCGACGCGTCCCATGTGTCACTTCAAGACGAGCTGTCTTT	321
QY	241	CCGACGTGGAGGCTCTGTCTTCAGAGCTTCGAGGTCGCGCTGAAGCCCGGGGGACGCAATC	300
Db	322	CCGACGTGGAGGCTCTGTCTTCAGAGCTTCGAGGTCGCGCTGAAGCCCGGGGGACGCAATC	381
QY	301	TTCCTCTTTTGAACGGCAAGGACGTCCTGAGGCAACCCACCTGGGCCGAGAAGCGTGTGG	360
Db	382	TTCCTCTTTTGAACGGCAAGGACGTCCTGAGGCAACCCACCTGGGCCGAGAAGCGTGTGG	441
QY	361	CATGGCTCGAACCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGCGTGGCGGACG	420
Db	442	CATGGCTCGAACCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGCGTGGCGGACG	501
QY	421	GAGGCTCTCCCTGGGCAACGGGCGCAGGCTCTCTGGTCTGGGGGAGGACGCTCTCTGGGGCAG	480
Db	502	GAGGCTCTCCCTGGGCAACGGGCGCAGGCTCTCTGGTCTGGGGGAGGACGCTCTCTGGGGCAG	561
QY	481	AGTGGCGGAGCTTGCATCAAGCCTCAACTGCTGCTGTGATTGGAACAGCTTCATGACT	540
Db	562	AGTGGCGGAGCTTGCATCAAGCCTCAACTGCTGCTGTGATTGGAACAGCTTCATGACT	621
QY	541	GGCTCC	546
Db	622	GGCTCC	627

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Job time : 357 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:04:38 ; Search time 2353 Seconds

(without alignments)  
10057.500 Million cell updates/sec

Title: US-10-042-347-4

Sequence: 1 caccgcccacgcgcactcca.....acagctcatgactgcctcc 546

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 3470272 seqs, 21671516395 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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41: em_hugo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	100.0	546	6	AR193165
2	546	100.0	549	6	BD240882
3	546	100.0	549	6	AX100086
4	546	100.0	552	6	BD26741
5	546	100.0	552	6	AX395662
6	546	100.0	552	6	AX473835
7	546	100.0	552	6	BD081407
8	546	100.0	563	6	AR418652
9	546	100.0	786	6	AF282883
10	546	100.0	900	6	AX370851
11	546	100.0	1388	9	AK130835
12	546	100.0	2364	9	AK098216
13	546	100.0	2376	6	AX816106
14	546	100.0	2376	6	AX816108
15	546	100.0	3394	6	151045
16	546	100.0	3394	6	AX409531
17	546	100.0	3394	6	FUMCOL18AX
18	546	100.0	5408	9	AF018082
19	546	100.0	5929	9	AF018081
20	544.4	99.7	564	9	AF416592
21	544.4	99.7	2637	9	BC033715
22	538	98.5	555	9	AF184060
23	534	97.8	534	6	AR193166
24	534	97.8	537	6	AX100092
25	520	95.2	650	6	AX370853
26	426.2	78.1	552	6	BD272245
27	419.6	76.8	552	6	BD240900
28	418	76.6	555	6	AX39631
29	418	76.6	555	6	BD188111
30	418	76.6	829	6	AX39629
31	418	76.6	829	6	BD188110
32	381.2	69.8	552	10	AF257775
33	381.2	69.8	555	6	BD102800
34	381.2	69.8	555	6	BD128313
35	381.2	69.8	558	6	AR268609
36	381.2	69.8	565	6	AR100642
37	381.2	69.8	565	6	E34073
38	381.2	69.8	573	6	BD271283
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# ALIGNMENTS

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RESULT 1
LOCUS AR193165 546 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6346510.
ACCESSION AR193165
VERSION AR193165.1 GI:20239130
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 546)
AUTHORS O'Reilly M.S. and Folkman M. Judah.
TITLE Therapeutic angiogenic endostatin compositions
JOURNAL Patent: US 6346510-A 4 12-FEB-2002;
FEATURES Location/Qualifiers

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## source

1. 546  
/organism="unknown"  
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## ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 546;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGAGCTTCCAGCCGATGCTCCAGCTGTTGGCTCAACAGCCCTGTCA 60  
DB 1 CACAGCCACCGGAGCTTCCAGCCGATGCTCCAGCTGTTGGCTCAACAGCCCTGTCA 60  
QY 61 GGGCGCATGCGGGGCAATCCGCGGGCCGATTCAGATCTTCAGAGCGCGGGCCGTG 120  
DB 61 GGGCGCATGCGGGGCAATCCGCGGGCCGATTCAGATCTTCAGAGCGCGGGCCGTG 120  
QY 121 GGGCGCATGCGGGGCAATCCGCGGGCCGATTCAGATCTTCAGAGCGCGGGCCGTG 180  
DB 121 GGGCGCATGCGGGGCAATCCGCGGGCCGATTCAGATCTTCAGAGCGCGGGCCGTG 180  
QY 181 GTGCGCGGCGGACCGGACCGGACCGGATGCTCAACCTCAAGAGAGCTGTGTTT 240  
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DB 241 CCGAGCTGGAGAGCTGTTCTCAGGCTTGAAGGCTTCGTAAGCCCGGGGCAAGCATC 300  
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DB 301 TTCTCTTTGACGGCAAGAGAGCTCTGAGGACCCCACTGGCCCGGAGAGAGCTGTG 360  
QY 361 CATGCTCGAGCCGCAACCGGCGGAGGCTGACGAGAGCTATGTAAGCTGTGCGAG 420  
DB 361 CATGCTCGAGCCGCAACCGGCGGAGGCTGACGAGAGCTATGTAAGCTGTGCGAG 420  
QY 421 GAGGCTCCCTCGGCGGACCGGCGGAGGCTCTGCTGCGGGGCGAGGCTCTGCGGG 480  
DB 421 GAGGCTCCCTCGGCGGACCGGCGGAGGCTCTGCTGCGGGGCGAGGCTCTGCGGG 480  
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DB 481 AGTGCAGGAGCTGCTCATCAAGCTCATGCTGTGCTGTGATTTGAGAACACTTCAACT 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 2  
BD240882 549 bp DNA linear PAT 17-JUL-2003  
LOCUS Expression and export of angiogenesis inhibitors as immunofusions.  
DEFINITION BD240882  
ACCESSION BD240882  
VERSION BD240882.1 GI:33050652  
KEYWORDS JP 2002523036-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 549)  
AUTHORS Lo, K.W., Li, X., and Gillies, S.D.  
TITLE Expression and export of angiogenesis inhibitors as immunofusions  
JOURNAL Patent: JP 2002523036-A 2 30-JUL-2002;  
LEXIGEN PHARMACEUTICALS CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002523036-A/2  
PD 30-JUL-2002  
PR 25-AUG-1999 JP 2000566305  
PI KIM MING LO, YUE LI, STEPHEN D GILLIES  
PC C12N15/09, A61K31/711, A61K38/00, A61K39/395, A61K48/00, A61P7/00,

## FEATURES

PC A61P35/00,  
PC A61P43/00, C07K14/745, C07K14/78, C07K19/00, C12N5/10, C12P21/02,  
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CC endostatin  
FH Key Location/Qualifiers  
FT CDS (1)..(549).  
Location/Qualifiers

## ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 GAGGCTCCCTCGGCGGACCGGCGGAGGCTCTGCTGCGGGGCGAGGCTCTGCGGG 480  
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DB 481 AGTGCAGGAGCTGCTCATCAAGCTCATGCTGTGCTGTGATTTGAGAACACTTCAACT 540  
QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 3  
AX100086 549 bp DNA linear PAT 02-APR-2001  
LOCUS Sequence 4 from Patent WO0119989.  
DEFINITION AX100086  
ACCESSION AX100086  
VERSION AX100086.1 GI:13539061  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
AUTHORS Liang, H., Sim, K.L., Chang-Murad, A., Zhou, X., Madsen, J.,  
Boerner, R.J., Bermejo, L.L., Mistry, F.R., Shepard, S.R. and

TITLE Schrimsher, J. L.  
Method of producing and purifying endostatin?m protein  
JOURNAL Patent: WO 011989-A 4 22-MAR-2001;  
Entremed, Inc. (US)

FEATURES  
source location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CACAGCCACCGGACTTCCAGCCGCTGCTCCACCTGTTGCGCTCAACAGCCCGCTGCA 60
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QY 61 GCGGCGATGCGGCGCATCCGCGGCGCGACCTTCAGTGTCTCCAGCAGCGCGCGCTG 120
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QY 481 AGTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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QY 541 GCCTCC 546
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## RESULT 4

BD266741 552 bp DNA linear PAT 17-JUN-2003  
LOCUS Proteins that bind angiogenesis-inhibiting proteins, compositions  
DEFINITION BD266741.1 GI:33076509  
ACCESSION BD266741  
VERSION BD266741.1  
KEYWORDS JP 2002532068-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 552)  
AUTHORS Macdonald, N. J. and Sim, K. L.  
TITLE Proteins that bind angiogenesis-inhibiting proteins, compositions  
and methods of use thereof  
JOURNAL Patent: JP 2002532068-A 2 02-OCT-2002;

## COMMENT

ENTREMED INC  
OS Homo sapiens (human)  
PN JP 2002532068-A/2  
PD 02-OCT-2002  
PF 06-DEC-1999 JP 2000585271  
PR 04-DEC-1998 US 09/206059  
PI NICHOLAS J MACDONALD, KIM LEE SIM  
PC C12N15/09, A61K38/00, A61P9/00, A61P27/02, A61P29/00, A61P35/00, PC  
A61P43/00,

PC C07K14/705, G01N33/15, G01N33/50, G01N33/53, G01N33/566//A61K35/16, PC  
A61K45/00,  
PC A61K48/00, C12N15/00, A61K37/02  
CC Proteins that bind angiogenesis-inhibiting proteins, CC  
compositions and  
methods of use thereof

FEATURES  
source location/Qualifiers  
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/organism="Homo sapiens"  
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## ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 552;  
Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 541 GCCTCC 546

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## RESULT 5

AX395662

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 DEFINITION Sequence 30 from Patent WO0193897.  
 ACCESSION AX395662  
 VERSION AX395662.1 GI:21066471  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Sim, K.L. and Macdonald, N.J.  
 Angiostatin and endostatin binding proteins and methods of use  
 Patent: WO 0193897-A 30 13-DEC-2001;  
 Entremed, Inc. (US)

FEATURES  
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ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCAGCCGGTGTCCAGCTGGTGGCTCAACAGCCCTGTCA 60  
 DB 1 CACAGCCACCGGACCTTCAGCCGGTGTCCAGCTGGTGGCTCAACAGCCCTGTCA 60  
 QY 61 GCGGCGATGCGGGGCAATCCGCGGGCCGACCTTCAGTGTCTTCAGAGCGCGCGCTG 120  
 DB 61 GCGGCGATGCGGGGCAATCCGCGGGCCGACCTTCAGTGTCTTCAGAGCGCGCGCTG 120  
 QY 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 DB 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 QY 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 DB 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 QY 181 GTGGCGCGTGGCCAGCGCGGAGCGTGCCTGCACTTCAAGAGAGAGCTGTGTT 240  
 DB 181 GTGGCGCGTGGCCAGCGCGGAGCGTGCCTGCACTTCAAGAGAGAGCTGTGTT 240  
 QY 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGATCCGCTGAAGCCCGGGGCAAGCATC 300  
 DB 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGATCCGCTGAAGCCCGGGGCAAGCATC 300  
 QY 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGAGCCCGAGAGAGCTGTGG 360  
 DB 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGAGCCCGAGAGAGCTGTGG 360  
 QY 361 CATGCTGGAGCCCGCAACGGGGGAGGCTGACGAGAGCTACTGTGAGAGCTGGCGAG 420  
 DB 361 CATGCTGGAGCCCGCAACGGGGGAGGCTGACGAGAGCTACTGTGAGAGCTGGCGAG 420  
 QY 421 GAGGCTCCCTCGGCAAGGAGCTCTGCTGTGGGGGAGGAGCTCTGTGGGGCAG 480  
 DB 421 GAGGCTCCCTCGGCAAGGAGCTCTGCTGTGGGGGAGGAGCTCTGTGGGGCAG 480  
 QY 481 AGTGGCGGAGCTCCATCAACGCTTACATGTGTCTGATTTAGAGAAAGCTTCATGACT 540  
 DB 481 AGTGGCGGAGCTCCATCAACGCTTACATGTGTCTGATTTAGAGAAAGCTTCATGACT 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

RESULT 6  
 AX473835 552 bp DNA linear PAT 09-AUG-2002  
 LOCUS AX473835  
 DEFINITION Sequence 2 from Patent WO0230982.  
 ACCESSION AX473835  
 VERSION AX473835.1 GI:22208005  
 KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Sim, K.L. and Liang, H.  
 Angiogenesis-inhibiting peptides and proteins and methods of use  
 Patent: WO 0230982-A 2 18-APR-2002;  
 Entremed, Inc. (US)

FEATURES  
 source Location/Qualifiers  
 1..552  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCAGCCGGTGTCCAGCTGGTGGCTCAACAGCCCTGTCA 60  
 DB 1 CACAGCCACCGGACCTTCAGCCGGTGTCCAGCTGGTGGCTCAACAGCCCTGTCA 60  
 QY 61 GCGGCGATGCGGGGCAATCCGCGGGCCGACCTTCAGTGTCTTCAGAGCGCGCGCTG 120  
 DB 61 GCGGCGATGCGGGGCAATCCGCGGGCCGACCTTCAGTGTCTTCAGAGCGCGCGCTG 120  
 QY 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 DB 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 QY 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 DB 121 GGGCTGGGGGCACTTCGGGCTTCTGTCTGTGGGCTTGCAGAGCTCTTACAGCATC 180  
 QY 181 GTGGCGCGTGGCCAGCGCGGAGCGTGCCTGCACTTCAAGAGAGAGCTGTGTT 240  
 DB 181 GTGGCGCGTGGCCAGCGCGGAGCGTGCCTGCACTTCAAGAGAGAGCTGTGTT 240  
 QY 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGATCCGCTGAAGCCCGGGGCAAGCATC 300  
 DB 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGATCCGCTGAAGCCCGGGGCAAGCATC 300  
 QY 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGAGCCCGAGAGAGCTGTGG 360  
 DB 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGAGACCCCACTGAGCCCGAGAGAGCTGTGG 360  
 QY 361 CATGCTGGAGCCCGCAACGGGGGAGGCTGACGAGAGCTACTGTGAGAGCTGGCGAG 420  
 DB 361 CATGCTGGAGCCCGCAACGGGGGAGGCTGACGAGAGCTACTGTGAGAGCTGGCGAG 420  
 QY 421 GAGGCTCCCTCGGCAAGGAGCTCTGCTGTGGGGGAGGAGCTCTGTGGGGCAG 480  
 DB 421 GAGGCTCCCTCGGCAAGGAGCTCTGCTGTGGGGGAGGAGCTCTGTGGGGCAG 480  
 QY 481 AGTGGCGGAGCTCCATCAACGCTTACATGTGTCTGATTTAGAGAAAGCTTCATGACT 540  
 DB 481 AGTGGCGGAGCTCCATCAACGCTTACATGTGTCTGATTTAGAGAAAGCTTCATGACT 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

RESULT 7  
 BD081407 552 bp DNA linear PAT 27-AUG-2002  
 LOCUS BD081407  
 DEFINITION Fused protein containing angiostatin component and utilization thereof in antitumor therapy.  
 ACCESSION BD081407  
 VERSION BD081407.1 GI:22627010  
 KEYWORDS JP 2001518304-A/50.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 552)  
 AUTHORS Bolanowski, M.A., Caparon, M.H., Caspersen, G.F., Gregory, S.A.,  
 TITLE Klein, B.K. and McKearn, J.P.  
 JOURNAL Fused protein containing angiostatin component and utilization  
 thereof in antitumor therapy  
 Patent: JP 2001518304-A 50 16-Oct-2001;  
 GD SEARLE AND CO  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001518304-A/50  
 PD 16-Oct-2001  
 PF 30-SEP-1998 JP 2000513958  
 PR 01-Oct-1997 US 60/060609  
 PI MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN A  
 PI GREGORY, J.  
 PI BARBARA K KLEIN, JOHN P MCKEARN  
 PC C12N15/09,A61K38/00,A61K48/00,A61P9/10,A61P35/00,C07K14/52, PC  
 C07K14/56,  
 CC Fused protein containing angiostatin component and utilization  
 thereof in  
 antitumor therapy  
 CC Key Location/Qualifiers  
 FT source 1..552  
 FT Location/Qualifiers  
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 /organism="Homo sapiens (human)"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCGCGGTCTCCACCTGTTGGCTTCAACACCCCTGTCA 60  
 DB 1 CACAGCCACCGGACCTTCCAGCGCGGTCTCCACCTGTTGGCTTCAACACCCCTGTCA 60  
 QY 61 GGGCGCATGCGGGGCAATCCGCGGGGCGACCTTCACTGCTTCCAGCGCGGGGCGTGG 120  
 DB 61 GGGCGCATGCGGGGCAATCCGCGGGGCGACCTTCACTGCTTCCAGCGCGGGGCGTGG 120  
 QY 121 GGGCTGGCGGACCTTCCGCGCTTCTCTGCTTCCGCGCTTCCAGGACCTGTACAAGCATC 180  
 DB 121 GGGCTGGCGGACCTTCCGCGCTTCTCTGCTTCCGCGCTTCCAGGACCTGTACAAGCATC 180  
 QY 181 GTGGCGCGTCCGACCGCGGACCGGTGCCATGTCTCAACCTCAAGACCAAGCTGCTTTT 240  
 DB 181 GTGGCGCGTCCGACCGCGGACCGGTGCCATGTCTCAACCTCAAGACCAAGCTGCTTTT 240  
 QY 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGTTCCGCTGAAGCCCGGGGACGACATC 300  
 DB 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGTTCCGCTGAAGCCCGGGGACGACATC 300  
 QY 301 TTCTCTTTTGAACGCAAGGAGCTCTGAAGCACTTCAAGGAGGAGGCTGTGG 360  
 DB 301 TTCTCTTTTGAACGCAAGGAGCTCTGAAGCACTTCAAGGAGGAGGCTGTGG 360  
 QY 361 CATGGCTGGAGCCCAACGCGGCGAGGCTTCAAGGAGGAGGCTTCAAGGAGGAGGAGG 420  
 DB 361 CATGGCTGGAGCCCAACGCGGCGAGGCTTCAAGGAGGAGGCTTCAAGGAGGAGGAGG 420  
 QY 421 GAGGCTCCCTCGGCGACGAGGCTCTCGCTGCTGGGGGAGGAGGCTCTCGGGGGAG 480  
 DB 421 GAGGCTCCCTCGGCGACGAGGCTCTCGCTGCTGGGGGAGGAGGCTCTCGGGGGAG 480  
 QY 481 AGTGGCGGAGCTGCTCAAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 DB 481 AGTGGCGGAGCTGCTCAAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

DB 541 GCCTCC 546

RESULT 8  
 LOCUS AR431862 563 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 9 from patent US 6653098.  
 ACCESSION AR431862  
 VERSION AR431862.1 GI:40194022  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 563)  
 AUTHORS Violand, B.N. and Harding, E.I.  
 TITLE Method of producing mouse and human endostatin  
 JOURNAL Patent: US 6653098-A 9 25-NOV-2003;  
 FEATURES Location/Qualifiers  
 1..563  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 546; DB 6; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCCAGCGCGGTCTCCACCTGTTGGCTTCAACACCCCTGTCA 60  
 DB 6 CACAGCCACCGGACCTTCCAGCGCGGTCTCCACCTGTTGGCTTCAACACCCCTGTCA 65  
 QY 61 GGGCGCATGCGGGGCAATCCGCGGGGCGACCTTCACTGCTTCCAGCGCGGGGCGTGG 120  
 DB 66 GGGCGCATGCGGGGCAATCCGCGGGGCGACCTTCACTGCTTCCAGCGCGGGGCGTGG 125  
 QY 121 GGGCTGGCGGACCTTCCGCGCTTCTCTGCTTCCGCGCTTCCAGGACCTGTACAAGCATC 180  
 DB 126 GGGCTGGCGGACCTTCCGCGCTTCTCTGCTTCCGCGCTTCCAGGACCTGTACAAGCATC 185  
 QY 181 GTGGCGCGTCCGACCGCGGACCGGTGCCATGTCTCAACCTCAAGACCAAGCTGCTTTT 240  
 DB 186 GTGGCGCGTCCGACCGCGGACCGGTGCCATGTCTCAACCTCAAGACCAAGCTGCTTTT 245  
 QY 241 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGTTCCGCTGAAGCCCGGGGACGACATC 300  
 DB 246 CCCAGCTGGAGGCTCTGTTCTCAGGCTTGAAGGTTCCGCTGAAGCCCGGGGACGACATC 305  
 QY 301 TTCTCTTTTGAACGCAAGGAGCTCTGAAGCACTTCAAGGAGGAGGCTGTGG 360  
 DB 306 TTCTCTTTTGAACGCAAGGAGCTCTGAAGCACTTCAAGGAGGAGGCTGTGG 365  
 QY 361 CATGGCTGGAGCCCAACGCGGCGAGGCTTCAAGGAGGAGGCTTCAAGGAGGAGGAGG 420  
 DB 366 CATGGCTGGAGCCCAACGCGGCGAGGCTTCAAGGAGGAGGCTTCAAGGAGGAGGAGG 425  
 QY 421 GAGGCTCCCTCGGCGACGAGGCTCTCGCTGCTGGGGGAGGAGGCTCTCGGGGGAG 480  
 DB 426 GAGGCTCCCTCGGCGACGAGGCTCTCGCTGCTGGGGGAGGAGGCTCTCGGGGGAG 485  
 QY 481 AGTGGCGGAGCTGCTCAAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 DB 486 AGTGGCGGAGCTGCTCAAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 545  
 QY 541 GCCTCC 546  
 DB 546 GCCTCC 551

RESULT 9  
 LOCUS AF282883 786 bp mRNA linear PRI 14-JUN-2002  
 DEFINITION Homo sapiens multi-functional protein MFP mRNA, complete cds.

ACCESSION AF282883  
 VERSION AF282883.1 GI:21425750  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 786)  
 AUTHORS Dou, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-2000) R & D, Robinson Biotech Corp., 24634 Five Mile Road, Suite 24-26, Redford, MI 48239, USA  
 FEATURES  
 source  
 1..786  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 1..786  
 /note="antiangiogenic agent"  
 /codon\_start=1  
 /product="multi-functional protein MFP"  
 /protein\_id="AA05249.1"  
 /db\_xref="GI:21425751"  
 /translation="MSBNSGSGSGGGGVTIKKGSGSGSGGGRNDGAKPMGSGSGSGGVTTPKLYDGGSGSGSGSGSHRDPQVTLVNLVNLGSGMRGIRADPOCEQOARVAGTFRAPLISRLDLYSIYRADRAVPIVNLKDELFPSEALFSSSGEPKPGARIFSPDKDYLHPMPKQSVHSGSDPNSRRLTESYCEWT EAPATGQASLIGRLGSAASCHAYIVCTIENSPTMSK"

ORIGIN  
 Query Match 100.0%; Score 546; DB 9; Length 786;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACCGGACCTTCCAGCGGTCTCCAGCTGTTGCTCAACGCCCCCTGTCA 60  
 235 CACAGCCACCGGACCTTCCAGCGGTCTCCAGCTGTTGCTCAACGCCCCCTGTCA 294  
 61 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 120  
 295 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 354  
 121 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 180  
 355 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 414  
 181 GTGCGCGGTGCGGACCGGCGGCGGCTTCAGGCTTCAGGAGGGGCGGGCGG 240  
 415 GTGCGCGGTGCGGACCGGCGGCGGCTTCAGGCTTCAGGAGGGGCGGGCGG 474  
 241 CCGAGCTGAGAGCTCTGTTTCAAGGCTTCAGGCTTCAGGAGGGGCGGGCGG 300  
 475 CCGAGCTGAGAGCTCTGTTTCAAGGCTTCAGGCTTCAGGAGGGGCGGGCGG 534  
 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGACCCCACTGGCCCCCAAGAGAGGTGTG 360  
 535 TTCTCTTTGACGGGCAAGAGCTCTGAGGACCCCACTGGCCCCCAAGAGAGGTGTG 594  
 361 CATGGCTGGAAGCCCAAGGGCGGAGGCTGACCGAGAGCTGAGAGAGGTGTG 420  
 595 CATGGCTGGAAGCCCAAGGGCGGAGGCTGACCGAGAGCTGAGAGAGGTGTG 654  
 421 GAAGGCTCTCGGCGGAGGGGCGGCTCTCGGCTGGGGGGGAGGCTCTGGGGCG 480  
 655 GAAGGCTCTCGGCGGAGGGGCGGCTCTCGGCTGGGGGGGAGGCTCTGGGGCG 714  
 481 AGTGGCGGAGCTGACGAGCTTACATCGTGTCTGCAATTGAGAGAGCTTACGACT 540  
 715 AGTGGCGGAGCTGACGAGCTTACATCGTGTCTGCAATTGAGAGAGCTTACGACT 774  
 541 GCCTCC 546  
 775 GCCTCC 780

RESULT 10  
 AX370851  
 LOCUS AX370851 900 bp DNA linear PAT 01-MAR-2002  
 DEFINITION Sequence 12 from Patent WO0210372.  
 ACCESSION AX370851  
 VERSION AX370851.1 GI:19168980  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1  
 AUTHORS Chapman, P.W., de Luca, G. and Falcioia, L.  
 TITLE Method of producing functional protein domains  
 JOURNAL Patent: WO 0210372-A 12 07-FEB-2002;  
 Applied Research Systems ARS Holding S.A. (AN)  
 FEATURES  
 source  
 1..900  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="mRNA for mlgsp fused to COL18A1 exons 38-41 for pmd-HR#1"

ORIGIN  
 Query Match 100.0%; Score 546; DB 6; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-77;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAGCCACCGGACCTTCCAGCGGTCTCCAGCTGTTGCTCAACGCCCCCTGTCA 60  
 337 CACAGCCACCGGACCTTCCAGCGGTCTCCAGCTGTTGCTCAACGCCCCCTGTCA 396  
 61 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 120  
 397 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 456  
 121 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 180  
 457 GGGGGATGCGGGGATCCCGGGGCGGATTCAGGCTTCAGGAGGGGCGGGCGG 516  
 181 GTGCGCGGTGCGGACCGGCGGCGGCTTCAGGCTTCAGGAGGGGCGGGCGG 240  
 517 GTGCGCGGTGCGGACCGGCGGCGGCTTCAGGCTTCAGGAGGGGCGGGCGG 576  
 241 CCGAGCTGAGAGCTCTGTTTCAAGGCTTCAGGCTTCAGGAGGGGCGGGCGG 300  
 577 CCGAGCTGAGAGCTCTGTTTCAAGGCTTCAGGCTTCAGGAGGGGCGGGCGG 636  
 301 TTCTCTTTGACGGGCAAGAGCTCTGAGGACCCCACTGGCCCCCAAGAGAGGTGTG 360  
 637 TTCTCTTTGACGGGCAAGAGCTCTGAGGACCCCACTGGCCCCCAAGAGAGGTGTG 696  
 361 CATGGCTGGAAGCCCAAGGGCGGAGGCTGACCGAGAGCTGAGAGAGGTGTG 420  
 697 CATGGCTGGAAGCCCAAGGGCGGAGGCTGACCGAGAGCTGAGAGAGGTGTG 756  
 421 GAAGGCTCTCGGCGGAGGGGCGGCTCTCGGCTGGGGGGGAGGCTCTGGGGCG 480  
 757 GAAGGCTCTCGGCGGAGGGGCGGCTCTCGGCTGGGGGGGAGGCTCTGGGGCG 816  
 481 AGTGGCGGAGCTGACGAGCTTACATCGTGTCTGCAATTGAGAGAGCTTACGACT 540  
 817 AGTGGCGGAGCTGACGAGCTTACATCGTGTCTGCAATTGAGAGAGCTTACGACT 876  
 541 GCCTCC 546  
 877 GCCTCC 882

RESULT 11  
 AK130835

LOCUS	AK130835	1389 bp	mRNA	linear	PI 10-SEP-2000
DEFINITION	Homo sapiens cDNA FLJ27325 fis, clone TMS08226, highly similar to				
ACCESSION	AK130835	Collagen alpha 1(XVII) chain precursor.			
VERSION	AK130835.1	GI:34527728			
KEYWORDS	Oligo capping; fis (full insert sequence).				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Kawakami,B., Sugiyama,A., Takemoto,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morigata,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Nagai,K., Isogai,T. and Sugano,S.				
AUTHORS	1				
TITLE	MEDO human cDNA sequencing project				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1389)				
AUTHORS	Sugano,S. and Suzuki,Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (31-Jul-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:fldna@ms.u-tokyo.ac.jp; Tel:81-3-5449-5286, Fax:81-3-5449-5416)				
COMMENT	MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.				
FEATURES	Location/Qualifiers				
source	1..1388				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="TMS08226"				
	/tissue_type="Thymus"				
	/clone_1fb="TMS"				
	/note="cloning vector: pMERISFL3"				
ORIGIN					
Query Match	100.0%;	Score 546;	DB 9;	Length 1389;	
Best Local Similarity	100.0%;	Pred. No. 9,4e-78;			
Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CACAGCAGCCCGACCTTCCAGCCCGGTGCTCAACTGTTGGGTCAAGCCGCCCTGTCTA	60		
Db	671	CACAGCAGCCCGACCTTCCAGCCCGGTGCTCAACTGTTGGGTCAAGCCGCCCTGTCTA	730		
QY	61	GAGCGGAGTCGGGGGCAATCCGCGGGCCGACCTTCAGTGCCTTCCAGAGCGCGGGCCGTG	120		
Db	731	GAGCGGAGTCGGGGGCAATCCGCGGGCCGACCTTCAGTGCCTTCCAGAGCGCGGGCCGTG	790		
QY	121	GAGCGCGGGGACACTTTCGGGCGCTTCTCTGTCTCTGCGCGCTCGACGAGACTGTGACAGATC	180		
Db	791	GAGCGCGGGGACACTTTCGGGCGCTTCTCTGTCTCTGCGCGCTCGACGAGACTGTGACAGATC	850		
QY	181	GTCGCGCGTCCGACCGCGCAGCGTGTCCCAATGTCAACTCAAGAGACGAGCTGTGTT	240		
Db	851	GTCGCGCGTCCGACCGCGCAGCGTGTCCCAATGTCAACTCAAGAGACGAGCTGTGTT	910		
QY	241	CCCAAGTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGCGGACAGCATC	300		
Db	911	CCCAAGTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGCGGACAGCATC	970		
QY	301	TTCCTCTTACCGGCAAGACGCTCTTGAGGCACTCCACCTTGCGCCCAAGAGAGCTGTGG	360		
Db	971	TTCCTCTTACCGGCAAGACGCTCTTGAGGCACTCCACCTTGCGCCCAAGAGAGCTGTGG	1030		
QY	361	CATGCTCGACCCCAACGGGCGCAGGCTGACCGAGAGCTACGTGAGAGAGTGGCGACG	420		

Db	103	CATGGCTCGGAGCCCAAGGGGGGCAAGGCTGACCGAAGACTACTGTGAGACAGTGGCGAGC	109
Qy	421	GAGGCTCCCTCGGCGCAAGGGCCAGGCTCTCTCGCTGCTGGGGGGGCAAGCTCTGGGGCAG	480
Db	1091	GAGGCTCCCTCGGCGCAAGGGGGCAGGCTCTCTCTCGCTGCTGGGGGGGCAAGGCTCTGGGGCAG	1155
Qy	481	AGTGGCGGCGAGGTGCCTGACACCGCTTACATCGTCTGTCTGATTTAGAGAACGCTTACATGACT	540
Db	1151	AGTGGCGGCGAGGTGCCTGACACCGCTTACATCGTCTGTCTGATTTAGAGAACGCTTACATGACT	1210
Qy	541	GGCTCC 546	
Db	1211	GGCTCC 1216	
RESULT 12			
AK098216			
LOCUS			
DEFINITION	AK098216	2364 bp mRNA linear	PR1 15-JUL-2002
ACCESSION	AK098216	AK098216.1	GI:21758185
VERSION	AK098216.1	GI:21758185	
KEYWORDS		oligo capping; fis (full insert sequence).	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS			
1	Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuki,H., Hara,H., Sugiyama,T., Irie,R., Otsubi,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Magatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuo,Y., Nagai,K. and Isogai,T.		
TITLE		NEO human cDNA sequencing project	
JOURNAL		Unpublished	
REFERENCE		2 (Phases 1 to 2364)	
AUTHORS		Isogai,T. and Yamamoto,J.	
TITLE		Direct Submission	
JOURNAL		Submitted (04-JUL-2002) Takao Isogai, F.I.J. Project (HRI Team); 2-6-7 Kazuwa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:isogenom@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.	
COMMENT		Location/Qualifiers	
		1..2364	
FEATURES			
source		/organism="Homo sapiens"	
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		/note="Cloning vector: PME185FL3"	
ORIGIN			
Query Match		100.0%; Score 546; DB 9; Length 2364;	
Best Local Similarity		100.0%; Pred. No. 8.1e-78;	
Matches 546;		Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	CACAGCCACCGCACCTTCCAGCGGCTGCTCACTCGTGTGGCGCTCAACAGCCGCCCTGTCA	60
Db	1644	CACAGCCACCGCACCTTCCAGCGGCTGCTCACTCGTGTGGCGCTCAACAGCCGCCCTGTCA	1703
Qy	61	GGGGGAGGAGCGGGGAGCTCGGGGGGCGACCTTCAGAGTGGCTTCAGAGCGGGCGGGCGGTG	120





(8/11/19)  
Fench

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:00:58 ; Search time 335 Seconds  
(without alignments)  
6923.929 Million cell updates/sec

Title: US-10-042-347-4  
Perfect score: 546  
Sequence: 1 cacagccaccgcgacttcca.....acagcttcatactgctctcc 546

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002s:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	100.0	546	3	AAA27004 Human end
2	546	100.0	549	2	AAX77719 Human ang
3	546	100.0	549	3	AAZ51291 Human ang
4	546	100.0	549	3	AAA29884 Human ang
5	546	100.0	549	5	AA800867 Human gen
6	546	100.0	549	7	ABA00774 Human end
7	546	100.0	552	2	AAA53575 SEQ ID 50
8	546	100.0	552	3	AAA68203 Human end
9	546	100.0	552	3	AAAC62023 Nucleotid
10	546	100.0	552	5	AAAC8289 Human end
11	546	100.0	552	6	ABK50685 CDNA enco
12	546	100.0	555	4	AAI66529 Human vas
13	546	100.0	558	6	ABA99261 Human end
14	546	100.0	563	2	AAZ08750 Human end
15	546	100.0	816	3	AAA64013 DNA enco
16	546	100.0	900	6	ABK09977 Nucleotid
17	546	100.0	968	3	AAAC62025 Nucleotid
18	546	100.0	1564	6	ABQ76740 DNA enco
19	546	100.0	3394	2	AAAT84484 Human alp
20	546	100.0	3394	2	AAX78379 Human alp
21	546	100.0	3394	6	ABN95680 Gene #217
22	546	100.0	4551	6	ABN85301 Human col
23	546	100.0	4551	6	ABV94763 Human pan

24	546	100.0	4875	6	ABO54955 Human ova
25	546	100.0	5408	2	AAX77720 Human col
26	545	99.8	551	6	ABO81193 Human end
27	542.8	99.4	641	4	AAH79104 Human end
28	542.8	99.4	641	6	AAU55454 Specific
29	542.8	99.4	641	6	ABO76079 Anticance
30	542.8	99.4	641	6	AAI44000 Reproduc
31	538	98.5	555	9	ADE40255 Human NOV
32	534	97.8	534	3	AAA27005 Alternate
33	534	97.8	537	5	AA80868 Human gen
34	532.6	97.5	6462	3	AA64014 Nucleotid
35	520	95.2	650	6	ABK09978 Synthetic
36	426.2	78.1	552	3	AAZ50398 Human end
37	419.6	76.8	552	3	AAZ51309 Canine an
38	418	76.6	555	6	AAI46063 Canine en
39	418	76.6	828	6	AD540257 Human NOV
40	416.4	76.3	482	9	ADE40259 Human NOV
41	405.6	74.3	480	9	AAX79949 Endostati
42	381.2	69.8	555	2	AAX84635 Mouse end
43	381.2	69.8	555	5	AA88290 Murine en
44	381.2	69.8	558	4	AAI8701 Mouse end
45	381.2	69.8	558	4	AAI8701 Mouse end

## ALIGNMENTS

## RESULT 1

ID AAA27004 standard; DNA; 546 BP.

XX AAA27004;

DT 11-AUG-2000 (first entry)

XX Human endostatin gene.

XX Human; endothelial cell proliferation inhibitor; collagen XVIII;

XX angiogenesis inhibitor; anti-tumour; cytostatic; antiproliferative;

XX vasotropic; dermatological; ophthalmological; vulnery;

XX antiarteriosclerotic; antidiabetic; haemostatic; contriceptive;

XX ocular angiogenic disease; atherosclerosis; scleroderma;

XX myocardial angiogenesis; telangiectasia; angiodioma;

XX wound granulation, ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..546 /product= "Endostatin protein"

FT MO200026368-A2.

XX 11-MAY-2000.

XX 01-NOV-1999; 99WO-US025605.

XX 30-OCT-1998; 98US-0106343P.

XX 20-MAY-1999; 99US-00315689.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX O'reilly MS, Folkman MJ;

XX WPI; 2000-365617/31.

XX F-PEDB; AAY94323.

Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents.

Claim 10; Page 39; 68pp; English.

XX The present sequence encodes an endostatin protein which is the carboxy  
 CC terminal protein of human collagen XVIII. Recombinant mouse endostatin  
 CC (20 mg/kg) was administered subcutaneously to mice implanted with Lewis  
 CC lung carcinomas. There was tumour mass regression non-detectable levels  
 CC after 12 days of therapy due to the angiogenesis inhibitory activity of  
 CC endostatin. Thus the protein is useful for treatment of angiogenesis-  
 CC dependent cancers. The polynucleotide and polypeptide sequences of this  
 CC endostatin are useful for treating and diagnosis of tumours, ocular  
 CC angiogenic diseases, Osler-Weber syndrome, myocardial angiogenesis,  
 CC plaque neovascularisation, telangiectasia, haemophilic joints,  
 CC angioblastoma and wound granulation, for treatment of diseases related to  
 CC excessive or abnormal stimulation of endothelial cells e.g. intestinal  
 CC adhesions, atherosclerosis, scleroderma. The protein may also be useful  
 CC as a birth control agent by reducing or preventing uterine  
 CC vascularisation. The gene for endostatin may be isolated from cells or  
 CC tissue that express high levels of endostatin, eg. tumour cells, by  
 CC generating cDNA from mRNA using reverse transcriptase and then amplifying  
 CC the DNA sequence

XX Sequence 546 BP; 80 A; 196 C; 177 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 3; Length 546;

Best Local Similarity 100.0%; Pred. No. 5,1e-102;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGCGACTTTCAGCCGCGTCTCACTGTTGCGCTCAACAGCCCCCTTCTCA 60  
 Db 1 CACAGCCACCGCGACTTTCAGCCGCGTCTCACTGTTGCGCTCAACAGCCCCCTTCTCA 60  
 QY 61 GGGGCGATGCGGGGATCCCGCGGCGGACCTTCAGGCTCCACAGCGCGGCGCG 120  
 Db 61 GGGGCGATGCGGGGATCCCGCGGCGGACCTTCAGGCTCCACAGCGCGGCGCG 120  
 QY 121 GGGCTGGGCGGACCTTCCGCGCTTCTGCTCTGCGCTGCGCTGAGAGACTTCAAGCATC 180  
 Db 121 GGGCTGGGCGGACCTTCCGCGCTTCTGCTCTGCGCTGCGCTGAGAGACTTCAAGCATC 180  
 QY 181 GTGCGCGTGGCGGACCGCGGAGCGGTGCCATCTCACTCAAGAGAGACTGCTTT 240  
 Db 181 GTGCGCGTGGCGGACCGCGGAGCGGTGCCATCTCACTCAAGAGAGACTGCTTT 240  
 QY 241 CCCAGCTGGAGGCTCTTCTTCAAGGCTCTGAGGGTCCGCTGAGAGCGGCGGCGCATC 300  
 Db 241 CCCAGCTGGAGGCTCTTCTTCAAGGCTCTGAGGGTCCGCTGAGAGCGGCGGCGCATC 300  
 QY 301 TTCTCTTTGAGCGGAGAGAGTCTGAGAGCACTTGGCCCTCCAGAGAGAGGTGTG 360  
 Db 301 TTCTCTTTGAGCGGAGAGAGTCTGAGAGCACTTGGCCCTCCAGAGAGAGGTGTG 360  
 QY 361 CATGGCTCGGACCCCAAGCGGCGGAGCTGACCGAGAGCTACGTGAGCGTGGAG 420  
 Db 361 CATGGCTCGGACCCCAAGCGGCGGAGCTGACCGAGAGCTACGTGAGCGTGGAG 420  
 QY 421 GAGGCTCTCTCGGCGGAGCGGCGGAGCTCTGCTGCGGCGGCGGAGCTCTCTGGGCGAG 480  
 Db 421 GAGGCTCTCTCGGCGGAGCGGCGGAGCTCTGCTGCGGCGGCGGAGCTCTCTGGGCGAG 480  
 QY 481 AGTGCAGGAGCTGACATCAAGCTTCAATGCTCTGCAATGAGAGAGCTTCAATCACT 540  
 Db 481 AGTGCAGGAGCTGACATCAAGCTTCAATGCTCTGCAATGAGAGAGCTTCAATCACT 540  
 QY 541 GCGTCC 546  
 Db 541 GCGTCC 546

RESULT 2  
 AAX77719 standard; DNA; 549 BP.

ID AAX77719  
 AC AAX77719;  
 XX

DT 10-AUG-1999 (first entry)

XX Human endostatin DNA coding region fragment.

XX Plasmidogen; human; angiotensin; endostatin; gene therapy; vector;

XX anti-angiogenic; attenuation; cytoskeletal; anti-diabetic; ophthalmology;

XX tumour growth; solid tumour; diabetic retinopathy; retina; ss.

XX Homo sapiens.

XX MO9926480-A1.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-US024950.

XX 20-NOV-1997; 97US-00975424.

XX (GENE-) GENETIX PHARM INC.

XX (MAST) MASSACHUSETTS INST TECHNOLOGY.

XX Leboulch P, Pawlitz RJ, Bachelot T;

XX WPI, 1999-357696/30.

XX P-PSDB; AAY08693.

XX Anti-angiogenic gene therapy vectors.

XX Disclosure: Page 74; 83pp; English.

CC This invention describes a novel viral gene therapy vector comprising a  
 CC nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from  
 CC human or murine angiotensin, human or murine endostatin and angiotensin-  
 CC inhibiting fusions and fragments, where the viral vector is sufficiently  
 CC attenuated for use in human gene therapy. The products of the invention  
 CC have anti-angiogenic, cytoskeletal, anti-diabetic and ophthalmological  
 CC activity. The vector is used in gene therapy for inhibiting tumour growth  
 CC in humans harbouring a solid tumour. The vector expresses an anti-  
 CC angiogenic polypeptide. An additional use comprises treatment of diabetic  
 CC retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis  
 CC in the vicinity of the retina. The vector is administered to cells ex  
 CC vivo and then administered to the patient

Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 2; Length 549;

Best Local Similarity 100.0%; Pred. No. 5,1e-102;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGCGACTTTCAGCCGCGTCTCACTGTTGCGCTCAACAGCCCCCTTCTCA 60  
 Db 1 CACAGCCACCGCGACTTTCAGCCGCGTCTCACTGTTGCGCTCAACAGCCCCCTTCTCA 60  
 QY 61 GGGGCGATGCGGGGATCCCGCGGCGGACCTTCAGGCTCCACAGCGCGGCGCG 120  
 Db 61 GGGGCGATGCGGGGATCCCGCGGCGGACCTTCAGGCTCCACAGCGCGGCGCG 120  
 QY 121 GGGCTGGGCGGACCTTCCGCGCTTCTGCTCTGCGCTGCGCTGAGAGACTTCAAGCATC 180  
 Db 121 GGGCTGGGCGGACCTTCCGCGCTTCTGCTCTGCGCTGCGCTGAGAGACTTCAAGCATC 180  
 QY 181 GTGCGCGTGGCGGACCGCGGAGCGGTGCCATCTCACTCAAGAGAGACTGCTTT 240  
 Db 181 GTGCGCGTGGCGGACCGCGGAGCGGTGCCATCTCACTCAAGAGAGACTGCTTT 240  
 QY 241 CCCAGCTGGAGGCTCTTCTTCAAGGCTCTGAGGGTCCGCTGAGAGAGAGCTTCAATCACT 300  
 Db 241 CCCAGCTGGAGGCTCTTCTTCAAGGCTCTGAGGGTCCGCTGAGAGAGAGCTTCAATCACT 300  
 QY 301 TTCTCTTTGAGCGGAGAGAGTCTGAGAGCACTTGGCCCTCCAGAGAGAGGTGTG 360  
 Db 301 TTCTCTTTGAGCGGAGAGAGTCTGAGAGCACTTGGCCCTCCAGAGAGAGGTGTG 360

	CC	blood born tumours, tumour metastasis, benign tumours including
	CC	haemangiomas, acoustic neuromas, neurofibromas, trichomas and pyrogenic
	CC	granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases
	CC	e.g. diabetic retinopathy, rejection of prematurity, macular
	CC	dysplasia, corneal graft rejection, neovascular glaucoma, retrolental
	CC	fibroplasia, rubeosis and Osler-Weber syndrome; myocardial angiogenesis,
	CC	plaque neovascularisation, telangiectasia, haemophilic joints'
	CC	angioblastoma, wound granulation, and excessive or abnormal stimulation of
	CC	endothelial cells, intestinal cells, atherosclerosis, sclerodermal and
	CC	hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in
	CC	gene therapy. The present sequence is a cDNA encoding human endothelin
	CC	used in the construction of immunofusion containing human immunoglobulin
	CC	gamma (IgG) Fc fragment. Note: This sequence is stated in claim 12 as
	CC	being amino acid sequence of plasminogen fragment, however, the rest of
	CC	the specification refers to this sequence as being nucleotide sequence of
	CC	human endothelin
	XX	
SQ	Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;	
Query Match	100.0%; Score 546; DB 3; Length 549;	
Best Local Similarity	100.0%; Pred. No. 5.1e-102;	
Matches 546;	Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 CACAGCCATCGCGAATTTCAGCCGGTGTCTCACCTGTGTTGGCTCAACGCCCTGTGTCA	60
Db	1 CACAGCCATCGCGAATTTCAGCCGGTGTCTCACCTGTGTTGGCTCAACGCCCTGTGTCA	60
OY	61 GGCGGCATCGGGGGCATTCGCGGGGGGCGAACATCAGTGCTTCACAGGCGGGGCGGTG	120
Db	61 GGCGGCATCGGGGGCATTCGCGGGGGGCGAACATCAGTGCTTCACAGGCGGGGCGGTG	120
OY	121 GGGGCTGGCGGGGACACTTCCGCGCTTCTGTCTGTGCGCGCTGCAGAGACCTGTACAGATC	180
Db	121 GGGGCTGGCGGGGACACTTCCGCGCTTCTGTCTGTGCGCGCTGCAGAGACCTGTACAGATC	180
OY	121 GGGGCTGGCGGGGACACTTCCGCGCTTCTGTCTGTGCGCGCTGCAGAGACCTGTACAGATC	180
Db	121 GGGGCTGGCGGGGACACTTCCGCGCTTCTGTCTGTGCGCGCTGCAGAGACCTGTACAGATC	180
OY	181 GTGGCGCTGTCCGACCGCGAGCGGTGCCATGTGAACCTCAAGACGAGCTGTGTT	240
Db	181 GTGGCGCTGTCCGACCGCGAGCGGTGCCATGTGAACCTCAAGACGAGCTGTGTT	240
OY	181 GTGGCGCTGTCCGACCGCGAGCGGTGCCATGTGAACCTCAAGACGAGCTGTGTT	240
Db	181 GTGGCGCTGTCCGACCGCGAGCGGTGCCATGTGAACCTCAAGACGAGCTGTGTT	240
OY	241 CCAGAGCTGGGAGGCTCTGTTCTCAAGGCTCTGAAGGTCCTGTAAGCTCCGGGGGACGATC	300
Db	241 CCAGAGCTGGGAGGCTCTGTTCTCAAGGCTCTGAAGGTCCTGTAAGCTCCGGGGGACGATC	300
OY	241 CCAGAGCTGGGAGGCTCTGTTCTCAAGGCTCTGAAGGTCCTGTAAGCTCCGGGGGACGATC	300
Db	241 CCAGAGCTGGGAGGCTCTGTTCTCAAGGCTCTGAAGGTCCTGTAAGCTCCGGGGGACGATC	300
OY	301 TTTCCTTTGACGCGACAAGACGTCTCTGAGGCAACCACCTGAGCCCCAGAAGAGGTGTGG	360
Db	301 TTTCCTTTGACGCGACAAGACGTCTCTGAGGCAACCACCTGAGCCCCAGAAGAGGTGTGG	360
OY	301 TTTCCTTTGACGCGACAAGACGTCTCTGAGGCAACCACCTGAGCCCCAGAAGAGGTGTGG	360
Db	301 TTTCCTTTGACGCGACAAGACGTCTCTGAGGCAACCACCTGAGCCCCAGAAGAGGTGTGG	360
OY	361 CATGCTCTGGACCCCAAAGGGGCGAGGCTGACCGAGAACTCATCTGTGACGCTGGCGAAG	420
Db	361 CATGCTCTGGACCCCAAAGGGGCGAGGCTGACCGAGAACTCATCTGTGACGCTGGCGAAG	420
OY	421 GAAGCTCTCTGGGCGACGGGGCAAGGCTCTCTGTGCTGTGGGGGGGAGGCTCTTGGGGGAG	480
Db	421 GAAGCTCTCTGGGCGACGGGGCAAGGCTCTCTGTGCTGTGGGGGGGAGGCTCTTGGGGGAG	480
OY	421 GAAGCTCTCTGGGCGACGGGGCAAGGCTCTCTGTGCTGTGGGGGGGAGGCTCTTGGGGGAG	480
Db	421 GAAGCTCTCTGGGCGACGGGGCAAGGCTCTCTGTGCTGTGGGGGGGAGGCTCTTGGGGGAG	480
OY	481 AGTGGCGAGACTGTCATCAGCCTCATATCGTGTCTGTGACAAAGCTTCATGACT	540
Db	481 AGTGGCGAGACTGTCATCAGCCTCATATCGTGTCTGTGACAAAGCTTCATGACT	540
OY	541 GCCTTC 546	
Db	541 GCCTTC 546	
RESULT 4		
AAA29884	ID	AAA29884 standard; cDNA; 549 BP.
XX AC	AAA29884;	
XX DT	22-AUG-2000	(First entry)
DE	Human angiotensin inhibiting factor I encoding cDNA	

XX Human; angiogenesis inhibiting factor 1; IAF-1; tumour; antibody;  
 KW abnormal vessel disease; ss.  
 XX Homo sapiens.  
 XX CNI244536-A.  
 XX 16-FEB-2000.  
 XX 10-AUG-1998; 98CN-00117150.  
 XX 10-AUG-1998; 98CN-00117150.  
 XX (ONCO-) INST ONCOLOGY UNDER TUMOR HOSPITAL CHINE.  
 XX Yang Z, Guo W;  
 XX WPI: 2000-388168/34.  
 XX P-PSDB; AAY90771.  
 XX Angiogenesis inhibiting factor 1 and its derivative useful for treating  
 PT tumors.  
 XX Example 1; Fig 5; 41pp; Chinese.  
 XX The present sequence encodes an angiogenesis inhibiting factor (1),  
 CC designated IAF-1. The present invention also describes: (1) preparation  
 CC of (1) and its derivative; (2) an IAF binding acceptor and its  
 CC preparation; and (3) an IAF antibody. (1) is useful for preparing new  
 CC biological preparations for effectively treating various tumours and  
 CC abnormal-vessel diseases. The IAF antibody is preferably a polyclonal  
 CC antibody, mosaic antibody, single stranded antibody and human originated  
 CC antibody  
 XX  
 SQ Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 546; DB 3; Length 549;  
 Best Local Similarity 100.0%; Pred.No. 5.1e-102;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGACCTTCAGCCGCGTCCAGCTGGTCCGCTCAAGAGCCCTGTCA 60  
 DB 1 CACAGCCACCGGACCTTCAGCCGCGTCCAGCTGGTCCGCTCAAGAGCCCTGTCA 60  
 QY 61 GGGCGCATGCGGGGATCCGGGGCCGACCTTCAGTGTCTTCCAGAGCGCGCGTGTG 120  
 DB 61 GGGCGCATGCGGGGATCCGGGGCCGACCTTCAGTGTCTTCCAGAGCGCGCGTGTG 120  
 QY 121 GGGCTGGCGGGACCTTCGCGCTTCTGTCTGTGCGCTGAGAGCCTGTACAGCATC 180  
 DB 121 GGGCTGGCGGGACCTTCGCGCTTCTGTCTGTGCGCTGAGAGCCTGTACAGCATC 180  
 QY 181 GTGAGCGGCGGACCGGCGAGCGCGGATGTCATGTCATCAAGAGCAGTGTCTGT 240  
 DB 181 GTGAGCGGCGGACCGGCGAGCGCGGATGTCATGTCATCAAGAGCAGTGTCTGT 240  
 QY 241 CCAGCTGGAGGCTCTGTCTGAGGCTCTGAGGTCCTGTAAGCCCGGGGCAAGCATC 300  
 DB 241 CCAGCTGGAGGCTCTGTCTGAGGCTCTGAGGTCCTGTAAGCCCGGGGCAAGCATC 300  
 QY 301 TTCTCCCTTTGACGGGCAAGAGTCTGAGGCGACCCCACTTGGCCCAAGAGGCTGTGG 360  
 DB 301 TTCTCCCTTTGACGGGCAAGAGTCTGAGGCGACCCCACTTGGCCCAAGAGGCTGTGG 360  
 QY 361 CATGCTCGGACCCCAAGCGGCGAGGCTGACCGAGACTACTGTGAGAGCTGTGGAAG 420  
 DB 361 CATGCTCGGACCCCAAGCGGCGAGGCTGACCGAGACTACTGTGAGAGCTGTGGAAG 420  
 QY 421 GAGGCTCCCTCGGCGACGCGGCTCTGTGCTGTGCTGAGGCGGAGGCTCTGTGAGG 480  
 DB 421 GAGGCTCCCTCGGCGACGCGGCTCTGTGCTGTGCTGAGGCGGAGGCTCTGTGAGG 480

QY 481 AGTGGCGGAGCTCCATCAGCGCTTACATGCTGCTGATGAGAGAGCTTCATGACT 540  
 DB 481 AGTGGCGGAGCTCCATCAGCGCTTACATGCTGCTGATGAGAGAGCTTCATGACT 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546  
 RESULT 5  
 ID AAS00867  
 AC AAS00867 standard; DNA; 549 BP.  
 XX AAS00867;  
 XX 04-JUL-2001 (first entry)  
 DE Human gene fragment encoding Endostatin(TM) protein.  
 XX Human; Endostatin(TM); angiogenesis mediated disease; solid tumours;  
 KW blood borne tumour; leukaemia; tumour metastasis; benign tumour;  
 KW haemangioma; acoustic neuroma; neurofibroma; trachoma; rubecosis;  
 KW pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer;  
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;  
 KW retinopathy of prematurity; macular corneal graft rejection;  
 KW neovascular glaucoma; retrolental fibroplasia; Osler-Weber Syndrome;  
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;  
 KW haemophilic joint; angiofibroma; wound granulation; ds.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1. 549  
 FT CDS  
 FT /tag= d  
 FT /product= "Endostatin(TM)"  
 FT /note= "None of the above CDSs have start or stop codons"  
 FT /partial  
 FT CDS  
 FT 1. 546  
 FT /tag= c  
 FT /product= "Endostatin(TM) C-terminus minus 1"  
 FT /note= "Variant produced during fermentation reaction of  
 FT Pichia pastoris harbouring an expression plasmid  
 FT containing the present sequence"  
 FT 1. 543  
 FT /tag= b  
 FT /product= "Endostatin(TM) C-terminus minus 2"  
 FT /note= "Variant produced during fermentation reaction of  
 FT Pichia pastoris harbouring an expression plasmid  
 FT containing the present sequence"  
 FT 1. 540  
 FT /tag= a  
 FT /product= "Endostatin(TM) C-terminus minus 3"  
 FT /note= "Variant produced during fermentation reaction of  
 FT Pichia pastoris harbouring an expression plasmid  
 FT containing the present sequence"  
 PN W0200119989-A2.  
 XX 22-MAR-2001.  
 PD 14-SEP-2000; 2000WO-US025166.  
 PF 14-SEP-1999; 99US-0153698P.  
 PR (ENTR-) ENTREMED INC.  
 XX Liang H, Sim KL, Chang-Murad A, Zhou X, Madson J, Boerner R;  
 PI Bernejo IL, Mistry FR, Shepard SR, Schrimsher J;  
 XX WPI: 2001-244802/25.

DR P-PSDB; AAU00896, AAU00897, AAU00898, AAU00899.

XX Producing Endostatin protein for treating angiogenesis mediated diseases  
PT such as solid tumors, comprises recombinantly producing the protein using  
PT an expression system, and recovering and purifying the protein.

PS Claim 6, Page 29; 67pp; English.

XX The sequence encodes Human Endostatin(TM). The new method of the  
CC invention is useful for producing, recovering and purifying Endostatin  
CC (TM) from biological sources, such as biological fluids, tissues, cells,  
CC culture media, and fermentation media. Endostatin(TM) is useful for  
CC treating angiogenesis mediated diseases such as solid tumors, blood  
CC borne tumors, leukemias, tumor metastases, benign tumors, e.g.  
CC haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic  
CC e.g., diabetic retinopathy, retinopathy of prematurity, macular  
CC degeneration, corneal graft rejection, neovascular glaucoma, colon  
CC cancer, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, colon  
CC haemophilic joints, angiodioma, and wound granulation. Endostatin(TM)  
CC is also useful for treating disease of excessive or abnormal stimulation  
CC of endothelial cells such as intestinal adhesions, atherosclerosis, and  
CC scleroderma and hypertrophic scars. Higher yields of more purified, and  
CC biologically active Endostatin(TM) are obtained by the new method.  
CC Endostatin(TM) can be stored in buffers for extended periods of time, and  
CC also subjected to lyophilisation, while preserving biological activity.  
CC Centrifugation of broth from fermentation steps in production is avoided,  
CC preventing unwanted potential cellular lysis and contamination with  
CC additional proteins, pigments, enzymes and other cellular chemicals and  
CC debris

XX Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 5; Length 549;  
Best Local Similarity 100.0%; Pred. No. 5.1e-102;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CACAGCAGCGGAGCTTCCAGCGGCTCCACCTGAGTTCGCTCAACAGCCCTCTGTCA 60
DB 1 CACAGCAGCGGAGCTTCCAGCGGCTCCACCTGAGTTCGCTCAACAGCCCTCTGTCA 60
QY 61 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCAGTTCGCTCAACAGCCCTCTGTCA 120
DB 61 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCAGTTCGCTCAACAGCCCTCTGTCA 120
QY 121 GGGCTGCGGGGATCTTCCGCGCTTCCTGCTCCGCGCTGAGAGCTGTAGAGCATC 180
DB 121 GGGCTGCGGGGATCTTCCGCGCTTCCTGCTCCGCGCTGAGAGCTGTAGAGCATC 180
QY 181 GGGCGCGTGCAGCGGCGGAGCGGCTGCTCAACCTGAGAGAGAGCTGTCTTT 240
DB 181 GGGCGCGTGCAGCGGCGGAGCGGCTGCTCAACCTGAGAGAGAGCTGTCTTT 240
QY 241 CCAAGCTGAGAGGCTGTCTCAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 300
DB 241 CCAAGCTGAGAGGCTGTCTCAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 300
QY 301 TTTCTCTTTTGAAGGAGAGCTCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 TTTCTCTTTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 AGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 AGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

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QY 541 GCCTCC 546  
DB 541 GCCTCC 546

RESULT 6  
ABA00774  
ID ABA00774 standard; cDNA; 549 BP.  
XX  
AC ABA00774;  
XX  
DT 18-MAR-2003 (first entry)  
XX  
DE Human endostatin coding sequence.

XX Gene; human; plasminogen; angiotensin; neovascularisation;  
XX kringle domain; cell proliferation; viral vector; replication-defective;  
XX cancer; tumour; ss.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
XX CDS 1..549  
XX FT /\*tag= a  
XX FT /product= "Endostatin"

XX MO200288173-A2.  
XX  
XX PD 07-NOV-2002.  
XX  
XX PF 29-APR-2002; 2002MO-US013461.  
XX  
XX PR 30-APR-2001; 2001US-0287673P.  
XX  
XX ER 05-APR-2002; 2002US-0370634P.

XX (CELL-) CELL GENESYS INC.

XX Chang B, Wu W, Macarthur J, Patel S, Jooss K, Mendez M,  
XX WPI; 2003-129131/12.  
XX DR P-PSDB; AAG79753.

XX New recombinant viral vector expressing human angiotensin useful for  
XX inhibiting angiogenesis in a mammalian subject with cancer or tumor.  
XX  
XX PS Example 4, Page 80-82; 83pp; English.

XX This sequence encodes endostatin. Endostatin is a 20 kD C-terminal  
XX fragment of collagen XVIII that inhibits angiogenesis. The endostatin  
XX coding sequence may be used in the recombinant viral vector of the  
XX invention for obtaining angiotensin activity. The vector comprises a  
XX promoter capable of expressing human angiotensin operably linked to a  
XX structural gene encoding one or more domains of human angiotensin. The  
XX vector, which may be a replication-defective viral vector, is useful for  
XX inhibiting angiogenesis in a mammal, especially with cancer or a tumour.  
XX Note: This sequence is given incorrectly in the sequence listing of the  
XX specification as an amino acid sequence

XX Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 7; Length 549;  
Best Local Similarity 100.0%; Pred. No. 5.1e-102;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CACAGCAGCGGAGCTTCCAGCGGCTCCACCTGAGTTCGCTCAACAGCCCTCTGTCA 60
DB 1 CACAGCAGCGGAGCTTCCAGCGGCTCCACCTGAGTTCGCTCAACAGCCCTCTGTCA 60
QY 61 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCAGTTCGCTCAACAGCCCTCTGTCA 120
DB 61 GGGCGCATGCGGGGATCCGCGGGGCGAGCTTCAGTTCGCTCAACAGCCCTCTGTCA 120

```

	CC	interferon-inducible protein and platelet-derived growth factor receptor tyrosine kinase activity. The multifunctional protein may also have other functions.
	CC	angiogenic and/or anti-tumor activity. The multifunctional protein may also have other functions.
	CC	exhibit useful properties such as having similar or greater biological activity than compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties.
	CC	The proteins can be used for treating an angiogenic-mediated disease, e.g., cancer, diabetic retinopathy, macular degeneration, or arthritis.
	CC	They can also be used for inhibiting the production of tumor cells characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma.
	CC	in a patient and for inhibiting tumor growth. The present sequence is used in the course of the invention
SQ	XX	Sequence 552 BF: 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;
		Query Match 100.0%; Score 546; DB 2; Length 552; Best Local Similarity 100.0%; Freqd. No.5.1e-102; Matches 546; Conservative 0%; Indels 0; Gaps 0
QY		1 CACAGCACCGGCACTTCAGCGGGTGTGCATCGTGTTGCCCTCAACAGCCCCCTGTCA 60     
Db		1 CACAGCACCGGCACTTCAGCGGGTGTGCATCGTGTTGCCCTCAACAGCCCCCTGTCA 60
QY		61 GGCGGCAATCGGGGCAATCGCGGGGCGAATTCAAGTAGTTCACAGCAGCGGGGCGGTG 120     
Db		61 GGCGGCAATCGGGGCAATCGCGGGGCGAATTCAAGTAGTTCACAGCAGCGGGGCGGTG 120
QY		121 GGAGTGGCGGGGCACTTTCGCGCGCTTCTGTCTCGCGCTGACAGGAACCTGTACAGCATC 180     
Db		121 GGAGTGGCGGGGCACTTTCGCGCGCTTCTGTCTCGCGCTGACAGGAACCTGTACAGCATC 180
QY		181 GTGCGCTGTCGACCGCGAGACCGCTGCGCAATGCTTAACCTCAGAGCAGAGCGCTGTT 240     

241 CCCAGCTGGAGGCTCTGTCTCAGGCTGAGGATCCGTCCGTGAAGCCCGGGCACCATC 300

[illegible][illegible]

RESULT 8  
AAA68203  
ID AAA68203 standard; cDNA; 552 BP.  
XX  
AC AAA68203;  
XX

DT 27-Oct-2000 (first entry)  
XX  
XX Human endostatin cDNA sequence.  
DE  
XX Angiogenesis-inhibiting protein receptor; angioestatin;  
KW angiogenesis; plasminogen; laminin; treatment; wound healing; solid tumour  
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;

KW	cerebral collateral, arteriovenous malformation; rubecsis; cancer;
KV	diabetic retinopathy; arthritis; wound healing; peptic ulcer;
KW	Helicobacter related disease; fracture; cat scratch fever; ss.
OS	Homo sapiens.
PN	WO200032631-A2.
XX	
XX	
PD	08-JUN-2000.
XX	
PF	06-DEC-1999; 99WO-US028897.
XX	
PR	04-DEC-1998; 98US-00206059.
XX	
PA	(ENTR-) ENTREMED INC.
PI	Macdonald NU, Sim KL;
DR	WPI; 2000-412290/35.
XX	
PT	New angiogenesis-inhibiting protein receptors, useful in methods for
PT	treating diseases and processes that are mediated by angiogenesis, such
PT	as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.
PS	Disclosure; Page 86; 100pp; English.
XX	

Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;

The invention relates to angiogenesis-inhibiting protein receptors, and the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, foetal and embryonal development and the formation of the corpus luteum, endometrium and placenta. Angiostatin is a protein (see AA16450 and AA68202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen AA16450). Angiostatin has the ability to inhibit angiogenesis'.

Angiostatin is also an angiogenesis inhibiting protein (see AA16451 and AA68203). Sequences AA68242 and AA16522 represent coding and protein sequences of human laminin. Laminin is an angiotensin binding protein, and some of the peptides of the invention share homology with regions of laminin. Peptides AA16455-B16521 (excluding AA16490) are the angiogenesis-inhibiting protein receptor fragments of the invention. CC peptides bind either angiotensin or endothelin and can be used in methods for treating diseases and processes that are mediated by angiogenesis, such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis, Crohn's disease, cerebral collagenosis, arteriovenous malformations, rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers, Kellidancer related diseases, fractures, placental and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628304-A628241 encode the peptides of the invention

	Query Match	100.0%;	Score 546;	DB 3	Length 552;
	Best Local Similarity	100.0%;	Pred. No. 5,1e-102;		
	Matches 546;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	CAAGACACCGGCACATTCCAGCCGAGTCTCACTGTGTGGCTCAACAGCCCCCTGTCA	60		
Db	1	CACAGCACCGGCACATTCCAGCCGAGTCTCACTGTGTGGCTCAACAGCCCCCTGTCA	60		
QY	61	GGGGGCATAGGGGGCATTCGGGGGGCCGACCTTCAGTCTTCAGACGGGCGGGCCGTG	120		
Db	61	GGGGGCATAGGGGGCATTCGGGGGGCCGACCTTCAGTCTTCAGACGGGCGGGCCGTG	120		
QY	121	GGGCTGGGGGCACCTTCCGAGCCTTCTCTCTCTCTGAGCGCTGGAGGACCTGTAAAGATC	180		
Db	121	GGGCTGGGGGCACCTTCCGAGCCTTCTCTCTCTCTGAGCGCTGGAGGACCTGTAAAGATC	180		
QY	181	GTGGCCCGGTGCCACCGGCGCAGCGTGTCCCATGTCAAACCTCAAGGACGAGCTGTGTT	240		
Db	181	GTGGCCCGGTGCCACCGGCGCAGCGTGTCCCATGTCAAACCTCAAGGACGAGCTGTGTT	240		
QY	241	CCCAAGTGGAGGCTCTGTCTCAGAGCTCGAGGGGTCCGCTGAAGCCCGGGGCAACGATC	300		
Db	241	CCCAAGTGGAGGCTCTGTCTCAGAGCTCGAGGGGTCCGCTGAAGCCCGGGGCAACGATC	300		

Db	241	CCGAGCTGGGAGGCTCTGTTCTTCAGGCTCTGAGGTCCTCCCTGAAACCCGGGGGACGATC	300
Qy	301	TTCTCTCTTTGAAGGCAAGACGTCTTGAAGGACCCCACTGGCCCAAGAAAGACGTGTG	360
Db	301	TTCTCTCTTTGAAGGCAAGACGTCTTGAAGGACCCCACTGGCCCAAGAAAGACGTGTG	360
Qy	361	CATGGCTCGAACCCCAACGGGGGCAAGGTGACCGAAGTACTGTGAAAGCTGGGGGACG	420
Db	361	CATGGCTCGAACCCCAACGGGGGCAAGGTGACCGAAGTACTGTGAAAGCTGGGGGACG	420
Qy	421	GAGGCTTCCTCGGCAAGGGCCAGGCTCTCTGCTGTGGGAGGACGCTCTGGGGGACG	480
Db	421	GAGGCTTCCTCGGCAAGGGCCAGGCTCTCTGCTGTGGGAGGACGCTCTGGGGGACG	480
Qy	481	AGTACCGCAGAGTCACATCAGCGCTCAATCGTCTGTGATTGAGAAACAGCTTCAATGCT	540
Db	481	AGTACCGCAGAGTCACATCAGCGCTCAATCGTCTGTGATTGAGAAACAGCTTCAATGCT	540
Qy	541	GCCCTCC	546
Db	541	GCCCTCC	546

[illegible]

CC endostatin and for identification of anti-angiogenic compounds in assays.  
 CC The endostatin protein is produced as a secreted, soluble protein which  
 CC needs no refolding, is stable in the fermentation broth and is produced  
 CC in large quantities. Streptomyces are amenable for cultivation in large  
 CC fermentations allowing for large quantities of soluble endostatin to be  
 CC produced

CC Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 3; Length 552;

Best Local Similarity 100.0%; Pred. No. 5.1e-102;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTGCA 60  
 DB 1 CACAGCCACCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTGCA 60  
 QY 61 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 120  
 DB 61 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 120  
 QY 121 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 180  
 DB 121 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 180  
 QY 181 GTGCGCGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 240  
 DB 181 GTGCGCGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 240  
 QY 241 CCGAGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 300  
 DB 241 CCGAGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 300  
 QY 301 TTCTCTTTGACGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 360  
 DB 301 TTCTCTTTGACGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 360  
 QY 361 CATGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 420  
 DB 361 CATGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 420  
 QY 421 GAGGCTGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 480  
 DB 421 GAGGCTGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 480  
 QY 481 AGTCCGCGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 540  
 DB 481 AGTCCGCGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 540  
 QY 541 GCCTCC 546  
 DB 541 GCCTCC 546

RESULT 10

AAC88289 standard; DNA; 552 BP.

AAC88289;

02-MAR-2001 (first entry)

Human endostatin coding sequence SEQ ID NO: 1.

XX Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken; cancer;

XX inflammation; angiogenesis-dependent disease; ds.

XX Homo sapiens.

XX MO200067771-A1.

XX 16-NOV-2000.

PF 02-MAY-2000; 2000MO-US012063.  
 XX 06-MAY-1999; 99US-0132907P.  
 PR 14-JUL-1999; 99US-00353333.  
 XX (BUEN-) BURNHAM INST.  
 XX Vuori K;  
 DR WPI: 2001-040937/05.  
 DR P-PSDB; AAB49379.  
 XX Endostatin peptide comprising at least four endostatin amino acid  
 PT residues are e.g. angiogenesis inhibitors for treating cancer and  
 XX diabetic retinopathy.  
 PS Disclosure; Page 111-112; 146pp; English.  
 CC The present invention provides endostatin peptides which can be used in  
 CC the modulation of angiogenesis. This is useful in the treatment of  
 CC cancer, inflammation, rheumatoid arthritis, chronic articular  
 CC rheumatism, psoriasis, disorders associated with inopportune invasion of  
 CC vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy  
 CC of prematurity, macular degeneration, corneal graft rejection,  
 CC retrolental fibroplasia, rubeosis, capillary proliferation in  
 CC atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent  
 CC diseases include Osler-Weber syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints and wound  
 CC granulation. In addition, the peptides can be used as birth control  
 CC agents  
 XX Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 U; 0 Other;  
 QY 1 CACAGCCACCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTGCA 60  
 DB 1 CACAGCCACCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTGCA 60  
 QY 61 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 120  
 DB 61 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 120  
 QY 121 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 180  
 DB 121 GGGGCGATGCGGGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 180  
 QY 181 GTGCGCGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 240  
 DB 181 GTGCGCGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 240  
 QY 241 CCGAGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 300  
 DB 241 CCGAGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 300  
 QY 301 TTCTCTTTGACGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 360  
 DB 301 TTCTCTTTGACGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 360  
 QY 361 CATGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 420  
 DB 361 CATGCTGGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 420  
 QY 421 GAGGCTGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 480  
 DB 421 GAGGCTGCTGCGGCACTTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 480  
 QY 481 AGTCCGCGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 540  
 DB 481 AGTCCGCGAGGCTGTCCAGCGGCTGTCCACTGTGTGGCTCAACAGCCCGCTG 540

the present sequence encodes human endostatin which is used to generate angiotensin-inhibiting peptides

PI Zhou Y;

PA (KANG-) KANGERWEI SCI & TECHNOLOGY DEV CO LTD

Zhou Y;

XX WPI; 2001-597614/68.  
 DR P-PSDB; AA678717.

XX Expression of recombinant human endothelial inhibin in Bichi yeast system.  
 PT Disclosure; Fig 1; 16pp; Chinese.

XX The present invention relates to a PCR based method, which can be used to  
 CC obtain the gene of human vascular endothelial inhibin from a human  
 CC mammary gland cDNA library by cloning, and the yeast expression plasmid  
 CC pPICZa-Endo containing the gene and its transformed *Pichia* engineering  
 CC strain GS115/pPICZa-Endo are constructed. The recombinant inhibin  
 CC expression is used to prepare recombinant human vascular endothelial  
 CC inhibin. The expression system features high Escherichia coli expression  
 CC levels, easy large-scale production, low cost and the modification  
 CC mechanism after protein maturation, folding and translation. The human  
 CC vascular endothelial inhibin has the bioactivity to suppress the  
 CC reproduction of vascular endothelial cells and the growth of tumor, so it  
 CC can be used as anticancer medicine. The present sequence is a coding  
 CC sequence described in the exemplification of the invention

XX Sequence 555 BP; 83 A; 198 C; 180 G; 94 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 4; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-102;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCAGCCGGTGTCTCCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 60  
 DB 4 CACAGCCACCGGCACTTCAGCCGGTGTCTCCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 63  
 QY 61 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 120  
 DB 64 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 123  
 QY 121 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 180  
 DB 124 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 183  
 QY 181 GTGCGCGTGTGCGGACCGGCGGACCGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 240  
 DB 184 GTGCGCGTGTGCGGACCGGCGGACCGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 243  
 QY 241 CCGAGCTGGAGGCTGTCTGTCTCAAGCTGTGAAGGCTCGTGAAGCCGGGGGCGGACATC 300  
 DB 244 CCGAGCTGGAGGCTGTCTGTCTCAAGCTGTGAAGGCTCGTGAAGCCGGGGGCGGACATC 303  
 QY 301 TTCTCCTTTGAAGGAGAGGAGCTGTGAAGGAGCCCACTGGGCCCAAGAGGCTGTG 360  
 DB 304 TTCTCCTTTGAAGGAGAGGAGCTGTGAAGGAGCCCACTGGGCCCAAGAGGCTGTG 363  
 QY 361 CATGGCTCGGACCCCAAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 420  
 DB 364 CATGGCTCGGACCCCAAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 423  
 QY 421 GAGGCTCCTCGGCGGAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 480  
 DB 424 GAGGCTCCTCGGCGGAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 483  
 QY 481 AGTGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTGAAGGAGCTGTG 540  
 DB 484 AGTGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTGAAGGAGCTGTG 543  
 QY 541 GCGTCC 546  
 DB 544 GCGTCC 549

RESULT 13  
 ABA9261  
 ID ABA9261 standard; cDNA; 558 BP.  
 XX

AC ABA9261;  
 XX 07-MAY-2002 (first entry)  
 DT  
 XX

DE Human endostatin cDNA fragment.

XX Endostatin; human; proliferation; blood vessel endothelium; regeneration;  
 KW tumour; blood vessel; treatment; amplification; ss.

XX Homo sapiens.

XX CN1177005-A.

XX 25-MAR-1998.

XX 10-SEP-1997; 97CN-00107112.

XX 10-SEP-1997; 97CN-00107112.

XX (XUG3/) XU G.

XX XU G, Ren M, Xu L;

XX WPI; 2002-106746/15.

DR P-PSDB; AA49503.

XX Gene clone of inhibitory factor for hyperplasia of inner blood vessel  
 PT cells in human body's real tumor, and its use in anti-tumor blood vessel  
 PT regeneration.

XX Disclosure; Page 4 (Disclosure); 6pp; Chinese.

XX This invention describes a novel preparation which inhibits the  
 CC proliferation of blood vessel endothelium and prevents the regeneration  
 CC activity of tumor blood vessels. The preparation can also be used as a  
 CC biological preparation in the treatment of tumours. This sequence encodes  
 CC the human endostatin gene described in the invention

XX Sequence 558 BP; 85 A; 197 C; 180 G; 96 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 6; Length 558;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-102;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGCCACCGGCACTTCAGCCGGTGTCTCCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 60  
 DB 7 CACAGCCACCGGCACTTCAGCCGGTGTCTCCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 66  
 QY 61 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 120  
 DB 67 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 126  
 QY 121 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 180  
 DB 127 GGGGCGATCGGGGCGATCCCGGGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 186  
 QY 181 GTGCGCGTGTGCGGACCGGCGGACCGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 240  
 DB 187 GTGCGCGTGTGCGGACCGGCGGACCGGCGGACCTTCAGCTGGTGTGCTCAAGAGCCCTGTCTCA 246  
 QY 241 CCGAGCTGGAGGCTGTCTGTCTCAAGCTGTGAAGGCTCGTGAAGCCGGGGGCGGACATC 300  
 DB 247 CCGAGCTGGAGGCTGTCTGTCTCAAGCTGTGAAGGCTCGTGAAGCCGGGGGCGGACATC 306  
 QY 301 TTCTCCTTTGAAGGAGAGGAGCTGTGAAGGAGCCCACTGGGCCCAAGAGGCTGTG 360  
 DB 307 TTCTCCTTTGAAGGAGAGGAGCTGTGAAGGAGCCCACTGGGCCCAAGAGGCTGTG 366  
 QY 361 CATGGCTCGGACCCCAAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 420  
 DB 367 CATGGCTCGGACCCCAAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 426  
 QY 421 GAGGCTCCTCGGCGGAGGCGGAGGCTGTGAAGGAGCTGTGAAGGAGCTGTG 480

Db 427 GAGGCTCCCTCGGCGCAAGGCTCTCTGCTGCTGGGGGCGAGGCTTCTTGGGCGAG 486  
 Qy 481 AGTCCGCGGAGCTGCTCATCAGGCTTACATCTGCTCTTGCAATTGAGAACAGCTTCATGACT 540  
 Db 487 AGTCCGCGGAGCTGCTCATCAGGCTTACATCTGCTCTTGCAATTGAGAACAGCTTCATGACT 546  
 Qy 541 GCTTCC 546  
 Db 547 GCTTCC 552

## RESULT 14

AA208750  
 ID AA208750 standard; cDNA, 563 BP.

AC AA208750;  
 XX  
 DT 03-NOV-1999 (first entry)  
 XX  
 DE Human endostatin cDNA isolate pMON20440.

XX Endostatin; inclusion body; expression; anticancer; antimetastatic;  
 KW angiogenesis; migration; proliferation; inhibition; collagen XVIII;  
 KM tumour; ss.

OS Homo sapiens.  
 XX  
 PN W09942486-A1.

PD 26-AUG-1999.

PF 19-FEB-1999; 99WO-US003271.

ER 23-FEB-1998; 98US-007587P.

PA (SEAR) SEARLE & CO G D.

PI Harding EI, Vieland BN;

DR WPI; 1999-527458/44.

XX Production of endostatin by refolding recombinant protein, useful as  
 PT anticancer and antimetastatic agent.

PS Claim 49; Page 47-48; 52pp; English.

CC A method has been developed for the production of endostatin (I). The  
 CC method comprises: (i) culturing host cells expressing the gene for (I);  
 CC (ii) recovering the gene product; (iii) refolding it at near neutral pH;  
 CC and (iv) isolating properly folded (I). (i) are inhibitors of  
 CC angiogenesis, by inhibiting migration and proliferation of endothelial  
 CC cells. The method is used to produce human or murine (I) from inclusion  
 CC bodies formed in recombinant bacteria. (i), the C-terminal fragment of  
 CC type alpha 1 collagen XVIII, is known to inhibit growth of some  
 CC metastases and primary tumours. The present sequence represents a cDNA  
 CC isolate containing a PCR fragment encoding human endostatin, including  
 CC the native human collagen XVIII C-terminal region

SQ Sequence 563 BP; 87 A; 198 C; 181 G; 97 T; 0 U; 0 Other;

Query Match 100.0%; Score 546; DB 2; Length 563;

Best Local Similarity 100.0%; Pred. No. 5, 1e-102;

Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACAGCCACCCGAGCTTCCAGCCGCTCTCAAGCTGTTGGCTCAACAGCCCTCTGCA 60  
 Db 6 CACAGCCACCCGAGCTTCCAGCCGCTCTCAAGCTGTTGGCTCAACAGCCCTCTGCA 65  
 Qy 61 GCGCGCATGCGGCGCATTCGCGGCGGCGGAGCTTCCAGTCTTCCAGGAGCGCGGCGGTG 120  
 Db 66 GCGCGCATGCGGCGCATTCGCGGCGGCGGAGCTTCCAGTCTTCCAGGAGCGCGGCGGTG 125

Qy 121 GGGCTGGGCGGCGCATCTTCGCGGCTTCTCTGCTGCGGCTGCAAGACCTTGACGATC 180  
 Db 126 GGGCTGGGCGGCGCATCTTCGCGGCTTCTCTGCTGCGGCTGCAAGACCTTGACGATC 185  
 Qy 181 GTGCGCGCTGCGGAGCCGCGCAGCCGTGCCATCTGCAACCTCAAGAGAGAGCTGCTTT 240  
 Db 186 GTGCGCGCTGCGGAGCCGCGCAGCCGTGCCATCTGCAACCTCAAGAGAGAGCTGCTTT 245  
 Qy 241 CCCAGCTGGAGGCTGCTGCTCAAGCTGAGGAGTCCGCTGAAAGCCCGGGGACGATC 300  
 Db 246 CCCAGCTGGAGGCTGCTGCTCAAGCTGAGGAGTCCGCTGAAAGCCCGGGGACGATC 305  
 Qy 301 TTCTCTTTTACGCGGAGAGAGCTGCTGAGGAGACCCCACTGAGCCCGGAGAGGCTGAG 360  
 Db 306 TTCTCTTTTACGCGGAGAGAGCTGCTGAGGAGACCCCACTGAGCCCGGAGAGGCTGAG 365  
 Qy 361 CATGCTCTGGAACCCCAAGCGGCGGAGGCTGACCGAGAGCTTGTGAGACGTGCGGAGC 420  
 Db 366 CATGCTCTGGAACCCCAAGCGGCGGAGGCTGACCGAGAGCTTGTGAGACGTGCGGAGC 425  
 Qy 421 GAGGCTCCCTCGGCGCAAGGCGGAGGCTCTGCTGCTGCTGGGGGCGAGGCTCTGGGGGAG 480  
 Db 426 GAGGCTCCCTCGGCGCAAGGCGGAGGCTCTGCTGCTGCTGGGGGCGAGGCTCTGGGGGAG 485  
 Qy 481 AGTCCGCGGAGCTGCTCATCAGGCTTACATCTGCTCTTGCAATTGAGAACAGCTTCATGACT 540  
 Db 486 AGTCCGCGGAGCTGCTCATCAGGCTTACATCTGCTCTTGCAATTGAGAACAGCTTCATGACT 545  
 Qy 541 GCTTCC 546  
 Db 546 GCTTCC 551

## RESULT 15

ID AAA64013  
 AAA64013 standard; DNA, 816 BP.

AC AAA64013;

DT 20-DEC-2000 (first entry)

DE DNA encoding a human angiogenesis inhibitor designated KED.

KW Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA;  
 KW tissue plasminogen activator; tumour; atherosclerosis; arthritis;  
 KW retinopathy; bronchial vascular congestion; inflammatory bowel disease;  
 KW adult respiratory distress syndrome; Castleman's disease; psoriasis;  
 KW hepatitis; aneurysm; renal disease; haemangioma; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..816  
 FT /\*tag = a  
 FT /product = "angiogenesis inhibitor KED"

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